

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 14:58:20 ; Search time 61 Seconds
(without alignments)
1148.718 Million cell updates/sec

Title: US-10-006-116A-194

Perfect score: 1374
Sequence: 1 MGLSTPLLCVGLGSLQATP.....GVYTYCKYVDWIRIMRN 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1374	100.0	248	3 AAB21304	Aab21304 Human KLK
2	1374	100.0	248	3 AAB24428	Aab24428 Human PRO
3	1374	100.0	248	3 AAB24032	Aab24032 Human PRO
4	1374	100.0	248	3 AAY99393	Aay99393 Human PRO
5	1374	100.0	248	4 AAM23994	Aam23994 Human EST
6	1374	100.0	248	4 AAB66142	Aab66142 Protein o
7	1374	100.0	248	6 ABO33635	Abo33635 Novel hum
8	1374	100.0	248	7 ABO44498	Abo44498 Human sec
9	1374	100.0	248	7 ABO33512	Abo33512 Novel hum
10	1374	100.0	248	7 ADC18063	Adc18063 Human PRO
11	1374	100.0	248	7 ADD70709	Add70709 Human sec
12	1374	100.0	248	7 ADD39786	Add39786 Human sec
13	1374	100.0	248	7 ADD70232	Add70232 Human sec
14	1374	100.0	248	7 ADD38353	Add38353 Human sec
15	1374	100.0	248	7 ADD39309	Add39309 Human sec
16	1374	100.0	248	7 ADD38832	Add38832 Human sec
17	1374	100.0	248	7 ADD40263	Add40263 Human sec
18	1374	100.0	248	7 ADE50484	Ade50484 Human sec
19	1374	100.0	248	7 ADE20096	Ade20096 Human sec
20	1374	100.0	248	7 ADE50007	Ade50007 Human sec
21	1374	100.0	248	7 ADE21565	Ade21565 Human sec
22	1367	99.5	248	6 AAO29516	Aao29516 Human kal
23	1301	94.7	254	3 AAB21303	Aab21303 Human KLK
24	1301	94.7	254	3 ABG66676	Abg66676 Human NOV
25	1019	74.2	184	3 AAB21301	Aab21301 Human KLK

26	811	59.0	162	2 AAY28642	Aay28642 Human sec
27	630.5	45.9	260	2 AAY32852	Aay32852 Human ser
28	630.5	45.9	260	2 AAY41744	Aay41744 Human PRO
29	630.5	45.9	260	2 AAY03220	Aay03220 Amino aci
30	630.5	45.9	260	3 AAB21322	Aab21322 Human neu
31	630.5	45.9	260	3 AAB44300	Aab44300 Human PRO
32	630.5	45.9	260	3 AAY51131	Aay51131 Human neu
33	630.5	45.9	260	4 AAU12369	Aau12369 Human PRO
34	630.5	45.9	260	4 AAB53087	Aab53087 Human ang
35	630.5	45.9	260	4 ABG23373	Abg23373 Novel hum
36	630.5	45.9	260	5 ABB84852	Abb84852 Human PRO
37	630.5	45.9	260	5 AAU81959	Aau81959 Human PRO
38	630.5	45.9	260	5 ABB95458	Abb95458 Human ang
39	630.5	45.9	260	6 ABO17813	Abo17813 Novel hum
40	630.5	45.9	260	6 ABO25246	Abo25246 Novel hum
41	630.5	45.9	260	6 ABU81067	Abu81067 Human PRO
42	630.5	45.9	260	6 ABU72252	Abu72252 Novel hum
43	630.5	45.9	260	6 ADA05702	Ada05702 Human NOV
44	630.5	45.9	260	6 ABU66767	Abu66767 Human PRO
45	630.5	45.9	260	6 ABU84932	Abu84932 Human sec

ALIGNMENTS

RESULT 1
AAB21304
ID AAB21304 standard; protein; 248 AA.

AC AAB21304;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human KLK-L5 protein #4.
XX
KW Human: KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
KW kallikrein-like protein; serine protease; cytostatic; cancer;
KW prostrate cancer.
XX
OS Homo sapiens.
XX
PN WO200053776-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-CA000258.
XX
PR 11-MAR-1999; 99US-0124260P.
PR 01-APR-1999; 99US-0127386P.
PR 21-JUL-1999; 99US-014919P.
XX
(MOUN) MOUNT SINAI HOSPITAL.
XX
PI Yousef GM, Diamandis EP;
XX
XX WPI; 2000-587440/55.
DR N-PSDB; AAA95944.
XX
XX New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
PT protein mediated disorders, especially cancer.
XX
XX Claim 12; Page 172; 184pp; English.

The present sequence is one of four alternatively spliced kallikrein-like proteins encoded by the human KLK-L4 gene. Kallikreins and kallikrein-like proteins are a subgroup of the serine protease enzyme family. They catalyse the selective cleavage of specific polypeptide precursors to release peptides with potent biological activity. Nucleic acids encoding kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-L6 have been isolated. The proteins are useful in the treatment, monitoring and diagnosis of cancers, especially prostate cancer. They can also be used to identify a substance that can associate with or mediate the biological activity of the proteins. Antibodies can be used

CC to treat conditions mediated by the kallikrein-like proteins

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1374; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGNSQPMQVGLFEGTSLRCGVLIDHRWLTA 60
 DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGNSQPMQVGLFEGTSLRCGVLIDHRWLTA 60

QY 61 AHCSSRWVRLGHSLSQLDWTEQIRHSGSVTHPGYLGASTSHEHDLRLRLPVRV 120
 DB 61 AHCSSRWVRLGHSLSQLDWTEQIRHSGSVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPNDCAATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYVGR 180
 DB 121 TSSVQPLPNDCAATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYVGR 180

QY 181 TSNMVCAGVPGQDACQDSGGPLVCGVQLGSLVSGVPGCGQDGI PGVYTYICKYVDM 240
 DB 181 TSNMVCAGVPGQDACQDSGGPLVCGVQLGSLVSGVPGCGQDGI PGVYTYICKYVDM 240

QY 241 IRIMNRNN 248
 DB 241 IRIMNRNN 248

RESULT 2

AAB24428
 ID AAB24428 standard; protein; 248 AA.

XX AC AAB24428;

XX DT 07-NOV-2000 (first entry)

XX DE Human PRO1303 protein sequence SEQ ID NO:203.

XX KW Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
 KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
 KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
 KW cytostatic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO200032221-A2.

XX PD 08-JUN-2000.

XX PF 30-NOV-1999; 99WO-US028313.

XX PR 01-DEC-1998; 98WO-US025108.

XX PR 16-DEC-1998; 98US-0112850P.

XX PR 12-JAN-1999; 99US-0115554P.

XX PR 08-MAR-1999; 99WO-US005028.

XX PR 12-MAR-1999; 99US-0123957P.

XX PR 28-APR-1999; 99US-0131445P.

XX PR 14-MAY-1999; 99US-0134287P.

XX PR 02-JUN-1999; 99WO-US012252.

XX PR 23-JUN-1999; 99US-0141037P.

XX PR 20-JUL-1999; 99US-0144758P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 13-SEP-1999; 99WO-US020594.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 15-SEP-1999; 99WO-US021547.

XX PR 05-OCT-1999; 99WO-US023089.

XX PR 29-OCT-1999; 99US-0162506P.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
 PI Goddard A, Godowski PU, Gurney AL, Klein RD, Kuo SS, Paoni NP;
 PI Smith V, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2000-412154/35.

XX N-PSDB; AAA77671.

XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
 PT and treating diagnosing a cardiovascular, endothelial or angiogenic
 PT disorders in mammals.

XX Claim 72; Fig 82; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides
 CC useful for preventing, diagnosing and treating diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder in mammals by
 CC modulating cell proliferation, angiogenesis and cardiovascularisation,
 CC and for identifying agonists and antagonists of these processes. The
 CC nucleic acids and the proteins they encode may be used in the prevention,
 CC treatment and diagnosis of diseases associated with inappropriate PRO
 CC expression such as cardiovascular, endothelial or angiogenic disorders in
 CC mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
 CC example, the nucleic acids (NCs) and vectors containing them and the PRO
 CC polypeptide may be used to treat disorders associated with decreased PRO
 CC expression. AAA77510 to AAA77721 and AAB24398 to AAB24435 represent
 CC nucleotide and protein sequences used in the exemplification of the
 CC present invention

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1374; DB 3; Length 248;

Best Local Similarity 100.0%; Pred. No. 3.8e-98;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLCVLGLSQAATPKIFNGTECGNSQPMQVGLFEGTSLRCGVLIDHRWLTA 60

DB 1 MGLSIFLLCVLGLSQAATPKIFNGTECGNSQPMQVGLFEGTSLRCGVLIDHRWLTA 60

QY 61 AHCSSRWVRLGHSLSQLDWTEQIRHSGSVTHPGYLGASTSHEHDLRLRLPVRV 120

DB 61 AHCSSRWVRLGHSLSQLDWTEQIRHSGSVTHPGYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPNDCAATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYVGR 180

DB 121 TSSVQPLPNDCAATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYVGR 180

QY 181 TSNMVCAGVPGQDACQDSGGPLVCGVQLGSLVSGVPGCGQDGI PGVYTYICKYVDM 240

DB 181 TSNMVCAGVPGQDACQDSGGPLVCGVQLGSLVSGVPGCGQDGI PGVYTYICKYVDM 240

QY 241 IRIMNRNN 248

DB 241 IRIMNRNN 248

RESULT 3

AAB24032

ID AAB24032 standard; protein; 248 AA.

XX AC AAB24032;

XX DT 25-JAN-2001 (first entry)

XX DE Human PRO1303 protein sequence SEQ ID NO:33.

XX KW Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 KW identification; tumorigenesis; anticancer; detection.

XX OS Homo sapiens.

XX PN WO200053750-A1.

XX PD 14-SEP-2000.

XX PF 02-DEC-1999; 99WO-US028551.
XX PR 08-MAR-1999; 99WO-US005028.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
XX PA (GETH) GENEMTECH INC.
XX PI Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX DR WPI; 2000-594320/56.
DR N-PSDB; AAC58114.
XX PT Antibodies specific for PRO polypeptides, used to diagnose and inhibit
PT the growth of tumors in mammals, and to identify inhibitors of PRO
PT polypeptide activity or expression.
XX PS Claim 61; Fig 24; 226pp; English.
XX CC The present invention describes an antibody that binds to a human protein
CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
CC PRO1927; PRO3567; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
CC PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
CC activity and can be used to diagnose tumours in mammals, by detecting
CC complex formation when the antibody is contacted with test cells.
CC Increased expression of genes encoding (I) can also be detected to
CC diagnose tumours. Agents which inhibit the activity of (I), especially
CC the antibodies, or an antisense oligonucleotide which hybridises to genes
CC encoding (I), can be used to inhibit tumour growth, preferably by
CC inducing cell death. Methods from the present invention can be used to
CC identify compounds which inhibit the biological activity of (I). AAC58019
CC to AAC58102 represent PCR primers and hybridisation probes used in
CC examples from the present invention for human PRO sequences. AAC58103 to
CC AAC58122 and AAC58123 to AAC58140 represent human PRO polynucleotide and
CC protein sequences given in the exemplification of the present invention
XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1374; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRVLTAA 60
DB 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRVLTAA 60

QY 61 AHCSGRYVWRLGHEHSLQDWMTEQIRHSGFVTHPGYLGASTSHEHDLRLRLRPVRV 120
DB 61 AHCSGRYVWRLGHEHSLQDWMTEQIRHSGFVTHPGYLGASTSHEHDLRLRLRPVRV 120

QY 121 TSSVQPLPLNDCATAGTCHVSGWITNHPNRPFDLLQCLNLSVSHATGCVYVPGRI 180
DB 121 TSSVQPLPLNDCATAGTCHVSGWITNHPNRPFDLLQCLNLSVSHATGCVYVPGRI 180

QY 181 TSNWCVAGVPGDQACQSGSGPLVCGVGLQGLVSGVSGPCQDGIPIGVYTYICKYVDW 240
DB 181 TSNWCVAGVPGDQACQSGSGPLVCGVGLQGLVSGVSGPCQDGIPIGVYTYICKYVDW 240

QY 241 IRIMERNN 248
DB 241 IRIMERNN 248

RESULT 4
AAAY9393
ID AAAY9393 standard; protein; 248 AA.
XX
AC AAAY9393;
XX
DT 08-AUG-2000 (first entry)

XX DE Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX OS Homo sapiens.
XX PN WO200012708-A2.
XX PD 09-MAR-2000.
XX PF 01-SEP-1999; 99WO-US020111.
XX PR 01-SEP-1999; 98US-0098716P.
PR 01-SEP-1999; 98US-0098749P.
PR 01-SEP-1999; 98US-0098750P.
PR 02-SEP-1999; 98US-0098803P.
PR 02-SEP-1999; 98US-0098821P.
PR 02-SEP-1999; 98US-0098843P.
PR 09-SEP-1999; 98US-0099536P.
PR 09-SEP-1999; 98US-0099596P.
PR 09-SEP-1999; 98US-0099598P.
PR 09-SEP-1999; 98US-0099602P.
PR 09-SEP-1999; 98US-0099642P.
PR 10-SEP-1999; 98US-0099741P.
PR 10-SEP-1999; 98US-0099754P.
PR 10-SEP-1999; 98US-0099763P.
PR 10-SEP-1999; 98US-0099792P.
PR 10-SEP-1999; 98US-0099808P.
PR 10-SEP-1999; 98US-0099812P.
PR 10-SEP-1999; 98US-0099815P.
PR 10-SEP-1999; 98US-0099816P.
PR 15-SEP-1999; 98US-0100385P.
PR 15-SEP-1999; 98US-0100388P.
PR 15-SEP-1999; 98US-0100390P.
PR 16-SEP-1999; 98US-0100584P.
PR 16-SEP-1999; 98US-0100627P.
PR 16-SEP-1999; 98US-0100661P.
PR 16-SEP-1999; 98US-0100662P.
PR 16-SEP-1999; 98US-0100664P.
PR 17-SEP-1999; 98US-0100683P.
PR 17-SEP-1999; 98US-0100684P.
PR 17-SEP-1999; 98US-0100710P.
PR 17-SEP-1999; 98US-0100711P.
PR 17-SEP-1999; 98US-0100919P.
PR 18-SEP-1999; 98US-0100930P.
PR 18-SEP-1999; 98US-0100848P.
PR 18-SEP-1999; 98US-0100849P.
PR 18-SEP-1999; 98US-0101014P.
PR 18-SEP-1999; 98US-0101068P.
PR 18-SEP-1999; 98US-0101071P.
PR 23-SEP-1999; 98US-0101279P.
PR 23-SEP-1999; 98US-0101471P.
PR 23-SEP-1999; 98US-0101472P.
PR 23-SEP-1999; 98US-0101474P.
PR 23-SEP-1999; 98US-0101475P.
PR 23-SEP-1999; 98US-0101476P.
PR 23-SEP-1999; 98US-0101477P.
PR 23-SEP-1999; 98US-0101479P.
PR 24-SEP-1999; 98US-0101738P.
PR 24-SEP-1999; 98US-0101741P.
PR 24-SEP-1999; 98US-0101743P.
PR 24-SEP-1999; 98US-0101915P.
PR 24-SEP-1999; 98US-0101916P.
PR 29-SEP-1999; 98US-0102207P.
PR 29-SEP-1999; 98US-0102240P.
PR 29-SEP-1999; 98US-0102307P.
PR 29-SEP-1999; 98US-0102330P.
PR 29-SEP-1999; 98US-0102331P.
PR 30-SEP-1999; 98US-0102484P.
PR 30-SEP-1999; 98US-0102487P.
PR 30-SEP-1999; 98US-0102570P.

PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
PR 06-OCT-1998; 98US-0103443P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
PR 07-OCT-1998; 98US-0103396P.
PR 07-OCT-1998; 98US-0103401P.
PR 08-OCT-1998; 98US-0103633P.
PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 14-OCT-1998; 98US-0104257P.
PR 14-OCT-1998; 98US-0104311P.
PR 20-OCT-1998; 98US-0104987P.
PR 20-OCT-1998; 98US-0105000P.
PR 20-OCT-1998; 98US-0105002P.
PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106364P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106913P.
PR 03-NOV-1998; 98US-0106933P.
PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
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PR 17-NOV-1998; 98US-0108802P.
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PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
XX (GETH) GENENTECH INC.
PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PI WPI; 2000-237871/20.
XX N-PSDB; AAA37075.
DR New mammalian DNA sequences encoding transmembrane, receptor or secreted
XX PRO polypeptides, useful for screening of potential peptide or small

PT molecule inhibitors of the relevant receptor/ligand interactions.
XX Claim 12; Fig 108; 773pp; English.
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AA99340 to AA99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding then have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX Sequence 248 AA;
SQ
Query Match 100.0%; Score 1374; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSIFLLLCVILGSLQAATPKIFNGTECGRNSQPWQVGLFPGTSLRCGGVLIDHRWVLT 60
Db 1 MGLSIFLLLCVILGSLQAATPKIFNGTECGRNSQPWQVGLFPGTSLRCGGVLIDHRWVLT 60
Qy 61 AHCSGSRYWFLGHSLSOLDWTQIRHSGFSVTHPGVGLGASTSHEHDLRLRLPLVRV 120
Db 61 AHCSGSRYWFLGHSLSOLDWTQIRHSGFSVTHPGVGLGASTSHEHDLRLRLPLVRV 120
Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGR 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGR 180
Qy 181 TSNMVCAGGVPGQDACQGDGSGPLVCGGLVGLVSGVSGVPGCGQDGI PGVTTYICKYVDM 240
Db 181 TSNMVCAGGVPGQDACQGDGSGPLVCGGLVGLVSGVSGVPGCGQDGI PGVTTYICKYVDM 240
Qy 241 IRMTIRNN 248
Db 241 IRMTIRNN 248
RESULT 5
AA023994
ID AA023994 standard; protein; 248 AA.
XX AC AA023994;
XX DT -12-OCT-2001 (first entry)
XX Human EST encoded protein SEQ ID NO: 1519.
DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX Homo sapiens.
OS WO200154477-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US002687.
XX 25-JAN-2001; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;


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XX DR WPI; 2001-476164/51.
XX N-ESDB; AAH98653.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use.
XX
XX Claim 20; Page 1048-1049; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a
XX protein of the invention
XX
XX SQ Sequence 248 AA;
XX
XX Query Match 100.0%; Score 1374; DB 4; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-98;
XX Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Qy 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
XX Db 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
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XX Qy 61 AHCSGSRYWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
XX Db 61 AHCSGSRYWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
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XX Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLOCLNLSIVSHATCHGVYPGRI 180
XX Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLOCLNLSIVSHATCHGVYPGRI 180
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XX Qy 181 TSNMVCAGGVPQDACQDGGPLVCGGVLAGLVSWSVGPCCGDIIPGVYTYICKYVDW 240
XX Db 181 TSNMVCAGGVPQDACQDGGPLVCGGVLAGLVSWSVGPCCGDIIPGVYTYICKYVDW 240
XX
XX Qy 241 IRMIMRNN 248
XX Db 241 IRMIMRNN 248
XX
XX RESULT 6
XX AAB66142
XX ID AAB66142 standard; protein; 248 AA.
XX
XX AC AAB66142;
XX
XX DT 02-APR-2001 (first entry)
XX
XX DE Protein of the invention #54.
XX
XX KW Secreted; transmembrane; gene therapy.
XX
XX OS Unidentified.
XX
XX PR WO200078961-A1.
XX
XX PD 28-DEC-2000.
XX
XX PF 18-FEB-2000; 2000WO-US004342.
XX
XX PR 23-JUN-1999; 99US-0141037P.
XX PR 20-JUL-1999; 99US-0144758P.
XX PR 26-JUL-1999; 99US-0145698P.
XX PR 01-SEP-1999; 99WO-US020111.
XX PR 29-OCT-1999; 99US-0162506P.
XX PR 30-NOV-1999; 99WO-US028313.
XX PR 02-DEC-1999; 99WO-US028551.
XX PR 16-DEC-1999; 99WO-US030095.
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PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR
PR (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong S,
XX Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PW, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
XX Claim 1; Fig 108; 787pp; English.
XX
XX The present invention relates to secreted and transmembrane proteins.
XX These proteins and the DNA encoding them may be used as hybridization
XX probes, in chromosome and gene mapping and in the generation of anti-
XX sense RNA and DNA. They may also be used to generate either
XX transgenic animals or knockout animals which are in turn useful for
XX development and screening of therapeutically useful reagents. The nucleic
XX acids may also be used in gene therapy
XX
XX SQ Sequence 248 AA;
XX
XX Query Match 100.0%; Score 1374; DB 4; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-98;
XX Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Db 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
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XX Qy 61 AHCSGSRYWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
XX Db 61 AHCSGSRYWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
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XX Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLOCLNLSIVSHATCHGVYPGRI 180
XX Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLOCLNLSIVSHATCHGVYPGRI 180
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XX Qy 181 TSNMVCAGGVPQDACQDGGPLVCGGVLAGLVSWSVGPCCGDIIPGVYTYICKYVDW 240
XX Db 181 TSNMVCAGGVPQDACQDGGPLVCGGVLAGLVSWSVGPCCGDIIPGVYTYICKYVDW 240
XX
XX Qy 241 IRMIMRNN 248
XX Db 241 IRMIMRNN 248
XX
XX RESULT 7
XX ABO33635
XX ID ABO33635 standard; protein; 248 AA.
XX
XX AC ABO33635;
XX
XX DT 17-SEP-2003 (first entry)
XX
XX DE Novel human secreted and transmembrane protein PRO1303.
XX
XX KW Human; secreted and transmembrane protein; PRO; angiogenesis;
XX endothelial cell proliferation; wound healing; immune response;
XX T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
XX cardiac insufficiency disorder; calcium flux; inflammation;
XX vascular endothelial growth factor-stimulated proliferation;
XX mammalian kidney mesangial cell proliferation; Berger disease;
XX nephropathy; Schanlein-Henoch purpura; celliac disease; Crohn's disease;
XX dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
XX pancreatic beta-cell precursor cell differentiation; thalassemias;
XX obesity; auditory hair cell regeneration; hearing loss; bone disorder;
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KW cartilage disorder; sports injury; arthritis.
XX Homo sapiens.
OS US2003073130-A1.
XX 17-APR-2003.
XX
XX 11-DEC-2001; 2001US-00015869.
XX
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098743P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
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PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
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PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
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PR 15-SEP-1998; 98US-0100383P.
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PR 16-SEP-1998; 98US-0100584P.
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PR 18-SEP-1998; 98US-0101068P.
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PR 24-SEP-1998; 98US-0101916P.
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PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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PR 07-OCT-1998; 98US-0103328P.
PR 07-OCT-1998; 98US-0103395P.
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PR 10-NOV-1998; 98US-0107783P.
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PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US0000219.

PR 06-JAN-2000; 2000WO-US0000376.
 PR 11-FEB-2000; 2000WO-US0003565.
 PR 18-FEB-2000; 2000WO-US0004342.
 PR 24-FEB-2000; 2000WO-US0005004.
 PR 02-MAR-2000; 2000WO-US0005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-585293/55.
 DR N-PSDB; ACD68378.

XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 1374; DB 6; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSIFLLLCVLGISOATPKIFNGTECGNSOPWQVGLFEQTSLRGGVLIDHRWLTA 60
 Db 1 MGLSIFLLLCVLGISOATPKIFNGTECGNSOPWQVGLFEQTSLRGGVLIDHRWLTA 60
 Qy 61 AHCSGRYWRVLRGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 Db 61 AHCSGRYWRVLRGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDQLQCLNLSIVSHATCHGVYFGRI 180
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 Db 181 TSNMVCAGVPGQDAGCGDSGLVCGGVTLQGLVSGSVCPGCGDGIKGVYVICKYVDW 240
 Qy 241 IRIMERNN 248
 Db 241 IRIMERNN 248

RESULT 8
 ABO44488

ID ABO44488 standard; protein; 248 AA.

XX ABO44488;

XX 01-OCT-2003 (first entry)

XX Human secreted/transmembrane protein PRO1303.

XX Human; secreted protein; transmembrane protein; PRO; vulnerable; cardiant;

KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
 KW adrenal cortical capillary; endothelial cell growth; wound healing;
 KW stimulated T-lymphocyte proliferation; immune response suppression;
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear cell;
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
 KW sports injury; arthritis.

XX Homo sapiens.

XX US2003044841-A1.

XX 06-MAR-2003.

XX 06-DEC-2001; 2001US-00006856.

XX 01-SEP-1998; 98US-00987116P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 01-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
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 PR 02-SEP-1998; 98US-0098843P.
 PR 02-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
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 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
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 PR 18-SEP-1998; 98US-0101068P.
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PR 02-OCT-1998; 98US-0102965P.
PR 06-OCT-1998; 98US-0103258P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
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PR 17-NOV-1998; 98US-0108787P.
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PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
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PR 17-NOV-1998; 98US-0108807P.
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PR 17-NOV-1998; 98US-0108925P.
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PR 18-NOV-1998; 98US-0108849P.
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PR 18-NOV-1998; 98US-0108852P.
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PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0123674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.

PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000176.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 24-AUG-2000; 2000WO-US023328.
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PR 10-NOV-2000; 2000WO-US030873.
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PR 01-MAR-2001; 2001WO-US006666.
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PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
XX Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
XX Williams PM, Wood WI;
XX WPI; 2003-492259/46.
XX N-PSDB; ACH04480.

Novel secreted and transmembrane polypeptides and polynucleotides
encoding them useful for treating various cardiac insufficiency
disorders, bone and/or cartilage disorders such as sports injuries and
arthritis.

Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGLSIFLLLCVLGSLQATPKIFNGTCGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
Db 1 MGLSIFLLLCVLGSLQATPKIFNGTCGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
Qy 61 AHCSGSRYWVRLGSHLSQLDWTBQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Db 61 AHCSGSRYWVRLGSHLSQLDWTBQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNRPFPDILLQCLNLSIVSHATCHGYPGRI 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNRPFPDILLQCLNLSIVSHATCHGYPGRI 180
Qy 181 TSNMVCAGGVPGDACCQDSGGPLVCGGLVGLWSGSGVPCGQDGIPOGVYTYCKYVDW 240
Db 181 TSNMVCAGGVPGDACCQDSGGPLVCGGLVGLWSGSGVPCGQDGIPOGVYTYCKYVDW 240
Qy 241 IRMIMRNN 248
Db 241 IRMIMRNN 248

RESULT 9
ABO33512


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Db 61 AHCSGRYVVRUGHSLSQDWTQIRHSFGFVTHPGYLGASTSHEDLRLRLPRV 120
Qy 121 TSSVQPLPNDCATAGTECHVSGWGIYTNHPNPPFDLLQCLNLSIVSHATCHGVYPGRI 180
Db 121 TSSVQPLPNDCATAGTECHVSGWGIYTNHPNPPFDLLQCLNLSIVSHATCHGVYPGRI 180
Qy 181 TSNMYCAGGVPGQDACQCGSGPLVCGGVLOGLVSGSVGPCQDGIPIGVYTYICKYVDW 240
Db 181 TSNMYCAGGVPGQDACQCGSGPLVCGGVLOGLVSGSVGPCQDGIPIGVYTYICKYVDW 240
Qy 241 IRMINRN 248
Db 241 IRMINRN 248

RESULT 11
ADD70709
ID ADD70709 standard; protein; 248 AA.
XX AC ADD70709;
XX DT 15-JAN-2004 (first entry)
XX DE Human secreted/transmembrane protein PRO1303.
XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX OS Homo sapiens.
XX FN US2003099625-A1.
XX PD 29-MAY-2003.
XX PF 12-DEC-2001; 2001US-00015386.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0099538P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
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PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
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PR 18-SEP-1998; 98US-0101014P.
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PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
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PR 30-SEP-1998; 98US-0102571P.
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PR 07-OCT-1998; 98US-0103314P.
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PR 07-OCT-1998; 98US-0103358P.
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PR 08-OCT-1998; 98US-0103678P.
PR 08-OCT-1998; 98US-0103679P.
PR 08-OCT-1998; 98US-0103711P.
PR 14-OCT-1998; 98US-0104257P.
PR 20-OCT-1998; 98US-0105000P.
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PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
PR 27-OCT-1998; 98US-0105807P.
PR 27-OCT-1998; 98US-0105881P.
PR 27-OCT-1998; 98US-0105882P.
PR 27-OCT-1998; 98US-0106062P.
PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 29-OCT-1998; 98US-0108500P.
PR 30-OCT-1998; 98US-0106464P.
PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
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PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
 PR 17-NOV-1998; 98US-0108787P.
 PR 17-NOV-1998; 98US-0108788P.
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 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108948P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR 22-DEC-1998; 98US-0113296P.
 PR 30-DEC-1998; 98US-0114223P.
 PR 05-JAN-1999; 99WO-US000106.
 PR 16-APR-1999; 99US-0129674P.
 PR 23-JUN-1999; 99US-0141037P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US020119.
 PR 29-OCT-1999; 99US-0162506P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 PR XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-874602/81.
 DR N-PSDB; ADD70708.
 XX
 XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
 PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
 XX
 PS Claim 12; SEQ ID NO 194; 553pp; English.
 XX
 XX The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 1374; DB 7; Length 248;
 Best Local Similarity 100.0%; Pred. No. 3.8e-98;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
 DB 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
 QY 61 AHCSGRYVRLGHEHLSQLDWTQIRHSGFVTHPGYLGASTSHEHDLRLRLPRV 120
 DB 61 AHCSGRYVRLGHEHLSQLDWTQIRHSGFVTHPGYLGASTSHEHDLRLRLPRV 120
 QY 121 TSSVQPLPLPNDCATAGTECHVSGMGTINHPRPFPDQLQCLNLSIVSHATCHGVYPERI 180
 DB 121 TSSVQPLPLPNDCATAGTECHVSGMGTINHPRPFPDQLQCLNLSIVSHATCHGVYPERI 180
 QY 181 TSNMVCAGGVPGQDACQSGDGGPLVCGGLVQGLVSGVPGCGQDGIPIGVYTYICKYVDW 240
 DB 181 TSNMVCAGGVPGQDACQSGDGGPLVCGGLVQGLVSGVPGCGQDGIPIGVYTYICKYVDW 240
 QY 241 IRMIMENN 248
 DB 241 IRMIMENN 248
 RESULT 12
 ADD39786
 ID ADD39786 standard; protein; 248 AA.
 XX AC ADD39786;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human secreted/transmembrane protein PRO1303.
 XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
 KW immune response; cardiac insufficiency disorder; calcium flux;
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
 KW Berger disease; nephropathy; Schönlain-Henoch purpura; coeliac disease;
 KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
 XX OS Homo sapiens.
 XX US2003083462-A1.
 XX PD 01-MAY-2003.
 XX PP 10-DEC-2001; 2001US-00013913.
 XX PR 05-JAN-1999; 99WO-US000106.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021194.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028551.
 PR 16-DEC-1999; 99WO-US030095.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005841.
 PR 02-MAR-2000; 2000WO-US006884.
 PR 15-MAR-2000; 2000WO-US013705.
 PR 17-MAY-2000; 2000WO-US014042.
 PR 22-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Deasoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski BJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoi NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-755122/71.
DR N-PSDB; ADD39785.
XX
XX New secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX
XX Claim 12; SEQ ID NO 194; 557pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides). Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimaeric molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. PRO is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours. PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1285, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g., arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence represents a PRO protein of the invention.
XX
XX Sequence 248 AA;
SQ

Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGLSTFLLCVLGSQAATPKIFNGTEGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
DB 1 MGLSIFLLCVLGSQAATPKIFNGTEGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
QY 61 AHCSGSRVWRLGHSLSQLDWTQEIQRSGFSVTHPGVYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSGSRVWRLGHSLSQLDWTQEIQRSGFSVTHPGVYLGASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDCAATAGTECHVSGWGI TNHPRNPDPDLLOCLNLSIVSHATCHGVYPCR 180
DB 121 TSSVQPLPLPNDCAATAGTECHVSGWGI TNHPRNPDPDLLOCLNLSIVSHATCHGVYPCR 180
QY 181 TSNMVCAGGVFGQDACQDSGGLVCGVQLGSLVSGVSGPCGQDGPVGYTYICKYVDW 240

DB 181 TSNMVCAGGVFGQDACQDSGGLVCGVQLGSLVSGVSGPCGQDGPVGYTYICKYVDW 240
QY 241 IRIMIRNN 248
DB 241 IRIMIRNN 248
RESULT 13
ADD70232
ID ADD70232 standard; protein; 248 AA.
XX
AC ADD70232;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane protein PRO1303.
XX
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
OS Homo sapiens.
XX
PN US2003054406-A1.
XX
PD 20-MAR-2003.
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PP 06-DEC-2001; 2001US-00006818.
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PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
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PR 09-SEP-1998; 98US-009596P.
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PR 10-SEP-1998; 98US-0099763P.
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PR 17-SEP-1998; 98US-0100710P.
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PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.

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PR	29-SEP-1998;	98US-0103240P.	PR	16-APR-1999;	99US-0129674P.	
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PR	29-SEP-1998;	98US-0102331P.	PR	26-JUL-1999;	99US-0145698P.	
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PR	30-SEP-1998;	98US-0102570P.	PR	29-OCT-1999;	99US-0162506P.	
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PR	07-OCT-1998;	98US-0103315P.	PR	24-FEB-2000;	2000WO-US005004.	
PR	07-OCT-1998;	98US-0103328P.	PR	02-MAR-2000;	2000WO-US005841.	
PR	07-OCT-1998;	98US-0103395P.	PR	15-MAR-2000;	2000WO-US006884.	
PR	07-OCT-1998;	98US-0103396P.	PR	17-MAY-2000;	2000WO-US013705.	
PR	07-OCT-1998;	98US-0103401P.	PR	22-MAY-2000;	2000WO-US014042.	
PR	08-OCT-1998;	98US-0103633P.	PR	30-MAY-2000;	2000WO-US014941.	
PR	08-OCT-1998;	98US-0103678P.	PR	02-JUN-2000;	2000WO-US015264.	
PR	08-OCT-1998;	98US-0103679P.	PR	23-AUG-2000;	2000WO-US023522.	
PR	14-OCT-1998;	98US-0104257P.	PR	24-AUG-2000;	2000WO-US023328.	
PR	20-OCT-1998;	98US-0104987P.	PR	08-NOV-2000;	2000WO-US030952.	
PR	20-OCT-1998;	98US-0105000P.	PR	10-NOV-2000;	2000WO-US030873.	
PR	20-OCT-1998;	98US-0105002P.	PR	01-DEC-2000;	2000WO-US032678.	
PR	21-OCT-1998;	98US-0105104P.	PR	28-FEB-2001;	2001WO-US006520.	
PR	22-OCT-1998;	98US-0105169P.	PR	01-MAR-2001;	2001WO-US006666.	
PR	22-OCT-1998;	98US-0105266P.	PR	01-JUN-2001;	2001WO-US017800.	
PR	26-OCT-1998;	98US-0105693P.	PR	20-JUN-2001;	2001WO-US019692.	
PR	26-OCT-1998;	98US-0105694P.	PR	29-JUN-2001;	2001WO-US021066.	
PR	27-OCT-1998;	98US-0105807P.	PR	09-JUL-2001;	2001WO-US021735.	
PR	27-OCT-1998;	98US-0105881P.	PR	04-SEP-2001;	2001US-00946374.	
PR	27-OCT-1998;	98US-0105882P.	XX			
PR	27-OCT-1998;	98US-0106062P.	PA	(GETH) GENENTECH INC.		
PR	28-OCT-1998;	98US-0106023P.	XX			
PR	28-OCT-1998;	98US-0106029P.	PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;		
PR	28-OCT-1998;	98US-0106030P.	PI	Gao W, God		

Qy 61 AHCSGSRYVRLGHSLSQLDWTQIRHSFGSVTHPGYLGASTSHEHDLRLRLPVRV 120 98US-0100711P.
Db 61 AHCSGSRYVRLGHSLSQLDWTQIRHSFGSVTHPGYLGASTSHEHDLRLRLPVRV 120 98US-0100913P.
Qy 121 TSSVQPLPLPNDCATAGTCHVSNGWITNNPRNPPDLLQCLNLSIVSHATCHGVYPGRI 180 98US-0100848P.
Db 121 TSSVQPLPLPNDCATAGTCHVSNGWITNNPRNPPDLLQCLNLSIVSHATCHGVYPGRI 180 98US-0100849P.
Qy 181 TSNMVCAGGVPCQACQDSCGPIVCGGVQLGLVSWGSVGPCGQDGPVVTYICKYVDM 240 98US-0101014P.
Db 181 TSNMVCAGGVPCQACQDSCGPIVCGGVQLGLVSWGSVGPCGQDGPVVTYICKYVDM 240 98US-0101016P.
Qy 241 IRMIMRNN 248 98US-0101071P.
Db 241 IRMIMRNN 248 98US-0101071P.
RESULT 14 98US-0101471P.
ADD38353 98US-0101472P.
ID ADD38353 standard; protein; 248 AA. 98US-0101474P.
XX 98US-0101475P.
AC ADD38353; 98US-0101476P.
XX 98US-0101477P.
DT 15-JAN-2004 (first entry) 98US-0101478P.
XX Human secreted/transmembrane protein PRO1303. 98US-0101479P.
XX Human; secreted; transmembrane protein; PRO; tumour; 98US-0101738P.
KW immune response; cardiac insufficiency disorder; calcium flux; 98US-0101741P.
KW umbilical vein endothelial cell; bone disorder; cartilage disorder; 98US-0101915P.
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity; 98US-0101916P.
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease; 98US-0102207P.
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia. 98US-0102207P.
XX 98US-0102307P.
XX 98US-0102330P.
XX 98US-0102331P.
XX 98US-0102487P.
XX 98US-0102487P.
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PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
PR 17-NOV-1998; 98US-0108788P.
PR 17-NOV-1998; 98US-0108801P.
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PR 17-NOV-1998; 98US-0108806P.
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PR 17-NOV-1998; 98US-0108867P.
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PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
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PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000105.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030099.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
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PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENE TECH INC.
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski RJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK;
PI Williams PM, Wood WJ;
XX WPI; 2003-787000/74.
DR N-PSDB; ADD38352.
XX
XX Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT thalassemias.
XX
XX Claim 12; SEQ ID NO 194; 556pp; English.
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
QY 61 AHCSGRYVWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEDHLRLRLPVRV 120
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QY 181 TSNMYCAGVPGQDACQGDGSGPLVCGGVLOGLVSGSVGRCGDDGIPGVYTYICKYVDW 240
DB 181 TSNMYCAGVPGQDACQGDGSGPLVCGGVLOGLVSGSVGRCGDDGIPGVYTYICKYVDW 240
QY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248
RESULT 15
ADD39309
ID ADD39309 standard; protein; 248 AA.
XX AC ADD39309;
XX 15-JAN-2004 (first entry)
XX Human secreted/transmembrane protein PRO1303.
KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpetiformis; Crohn's disease; thalassemia.
XX Homo sapiens.
OS US2003096954-A1.
PN 22-MAY-2003.
XX 07-DEC-2001; 2001US-00011671.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 09-SEP-1998; 98US-0098536P.
PR 09-SEP-1998; 98US-0099596P.
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PR 09-SEP-1998; 98US-0099642P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
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PR 10-SEP-1998; 98US-0099815P.
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PR 15-SEP-1998; 98US-0100385P.
PR 15-SEP-1998; 98US-0100388P.

PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
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PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
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PR 26-OCT-1998; 98US-0105693P.
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PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.

PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
PR 30-OCT-1998; 98US-0108500P.
PR 03-NOV-1998; 98US-0106464P.
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PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
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PR 03-NOV-1998; 98US-0106934P.
PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
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PR 17-NOV-1998; 98US-0108801P.
PR 17-NOV-1998; 98US-0108802P.
PR 17-NOV-1998; 98US-0108806P.
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PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108848P.
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PR 18-NOV-1998; 98US-0108850P.
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PR 18-NOV-1998; 98US-0108852P.
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PR 22-DEC-1998; 98US-0113296P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 98US-0114223P.
PR 16-APR-1999; 98US-0129674P.
PR 23-JUN-1999; 98US-0141037P.
PR 26-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 01-SEP-1999; 98US-0145698P.
PR 15-SEP-1999; 98US-0145698P.
PR 29-OCT-1999; 98US-0145698P.
PR 30-NOV-1999; 98US-0145698P.
PR 02-DEC-1999; 98US-0145698P.
PR 05-JAN-2000; 98US-0145698P.
PR 06-JAN-2000; 98US-0145698P.
PR 11-FEB-2000; 98US-0145698P.
PR 18-FEB-2000; 98US-0145698P.
PR 24-FEB-2000; 98US-0145698P.
PR 02-MAR-2000; 98US-0145698P.
PR 15-MAR-2000; 98US-0145698P.
PR 17-MAY-2000; 98US-0145698P.
PR 22-MAY-2000; 98US-0145698P.
PR 30-MAY-2000; 98US-0145698P.
PR 23-AUG-2000; 98US-0145698P.
PR 24-AUG-2000; 98US-0145698P.
PR 08-NOV-2000; 98US-0145698P.
PR 10-NOV-2000; 98US-0145698P.
PR 01-DEC-2000; 98US-0145698P.
PR 28-FEB-2001; 98US-0145698P.
PR 01-MAR-2001; 98US-0145698P.
PR 01-JUN-2001; 98US-0145698P.
PR 20-JUN-2001; 98US-0145698P.
PR 09-JUL-2001; 98US-0145698P.
PR 29-JUL-2001; 98US-0145698P.
PR 04-SEP-2001; 98US-0145698P.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Faoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-786999/74.
DR

DR N-PSDB; ADD39308.
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 12; SEQ ID NO 194; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT 60
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Qy 241 IRMIMENN 248
Db 241 IRMIMENN 248

Search completed: June 16, 2004, 15:04:50
Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:02:46 ; Search time 21 Seconds
(without alignments)
1135.976 Million cell updates/sec

Title: US-10-006-116a-194
Perfect score: 1374
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	622.5	45.3	260	2 I56559	neutropsin - mouse
2	569.5	41.4	248	2 S55066	trypsin (EC 3.4.21)
3	567	41.3	248	2 S55067	trypsin (EC 3.4.21)
4	561	40.8	231	1 TRPGTR	trypsin (EC 3.4.21)
5	555	40.4	243	2 A35871	trypsin (EC 3.4.21)
6	555	40.4	253	2 A53968	serine proteinase
7	553	40.2	246	2 B25528	trypsin (EC 3.4.21)
8	552	40.2	229	1 TRBOTR	trypsin (EC 3.4.21)
9	550	40.0	247	2 S13813	trypsin (EC 3.4.21)
10	546	39.7	247	1 TRDGC	trypsin (EC 3.4.21)
11	545	39.7	246	1 TRDGC	trypsin (EC 3.4.21)
12	544.5	39.6	247	2 TRD547	trypsin (EC 3.4.21)
13	543	39.5	246	1 TRRT1	trypsin (EC 3.4.21)
14	540	39.3	238	2 S31779	trypsin (EC 3.4.21)
15	533.5	38.8	247	2 S05494	trypsin (EC 3.4.21)
16	532	38.7	246	1 TRRT2	trypsin (EC 3.4.21)
17	527.5	38.4	261	2 A31136	tissue kallikrein
18	524	38.1	232	1 KQPG	tissue kallikrein
19	520.5	37.9	261	2 A25606	tissue kallikrein
20	519	37.8	246	2 JQ1471	trypsin (EC 3.4.21)
21	518	37.7	246	2 JQ1472	trypsin (EC 3.4.21)
22	518	37.7	261	2 A34079	tissue kallikrein
23	513.5	37.4	231	2 S31778	trypsin (EC 3.4.21)
24	513.5	37.4	239	2 A27207	tissue kallikrein
25	511.5	37.2	261	2 S45303	tissue kallikrein
26	510.5	37.2	261	1 NGMSG	7S nerve growth fa
27	508	37.0	242	2 S31775	trypsin (EC 3.4.21)
28	508	37.0	242	2 S31776	trypsin (EC 3.4.21)
29	503	36.6	260	2 A37938	tissue kallikrein

30	503	36.6	263	2 S15686	tissue kallikrein
31	502	36.5	259	2 B31136	tissue kallikrein
32	501	36.5	247	1 B25852	trypsin (EC 3.4.21)
33	499.5	36.4	241	2 S39048	trypsin (EC 3.4.21)
34	496.5	36.1	261	1 TRMSM5	tissue kallikrein
35	496	36.1	242	2 S49489	trypsin (EC 3.4.21)
36	495.5	36.1	257	2 S33772	tissue kallikrein
37	495.5	36.1	261	2 S01971	tissue kallikrein
38	494.5	36.0	247	1 A25852	trypsin (EC 3.4.21)
39	493	35.9	262	1 KQHU	tissue kallikrein
40	491.5	35.8	240	2 S39047	trypsin (EC 3.4.21)
41	491	35.7	256	1 NGMSA	7S nerve growth fa
42	490.5	35.7	229	1 TRDPS	trypsin (EC 3.4.21)
43	490.5	35.7	261	2 A41020	tissue kallikrein
44	489	35.6	244	2 A44284	tissue kallikrein
45	485.5	35.3	261	2 JB0236	tissue kallikrein

ALIGNMENTS

RESULT 1

I56559

neutropsin - mouse

C:Species: Mus musculus (house mouse)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000

C:Accession: I56559

J. Neurosci. 15, 5088-5097, 1995

A:Title: Expression and activity-dependent changes of a novel limbic-serine protease ge

A:Reference number: I56559; MUID:95348817; PMID:7623137

A:Accession: I56559

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-260 <RES>

A:Cross-references: GB:D30785; NID:g1648847; PIDN:BAA06451.1; PID:g1020091

C:Superfamily: trypsin; trypsin homology

P:33-252/Domain: trypsin homology <TRY>

Query Match 45.3%; Score 622.5; DB 2; Length 260;

Best Local Similarity 49.0%; Pred. No. 1.4e-43;

Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;

Qy	5	IFLLLCV---	LGLSQATPKIFNGTCGRNSQPVGLPBGTSRLRCGGVLIDHRWLTAA	61
Db	13	ILLFLFMGAWAGITRAQGGKILEGRCIPHSQPMQAALFQGRLLICGGVLVGDNRWLTAA	72	
Qy	62	HCSGSYVWRLGRHSLSQLDWTQIRHSGSPVTHPGVLGAS-TSHEHDLRLRLRPVRV	120	
Db	73	HCKKQKYSVRLGDHSLQSRDQPEQBIQVAQSIQHPCTVNSNPEDHSHIDMLRLQNSANL	132	
Qy	121	TSSVQPLPLPNDCATAGTECHVSGWGITHPRNPFPDQLQCLNLSIVSHATCHGVYFGR	180	
Db	133	GDKVKEVQLANLCPKVGQKCIISGWGTVPSPQENFNTLNCAEVKIVSQNKCRAYFGKI	192	
Qy	181	TSNWCAGVPGDQACQSGSGPLVCGGVLCGLVSGSVGCPQDQGIPIGVYTIKTYVDW	240	
Db	193	TEGMVCASSNGADTCQSGSGPLVCGDMLQGITSWGSDPCGKPEKPGVYTIKRYTTW	251	
Qy	241	IRMIMEN	247	
Db	252	IKKTMND	258	

RESULT 2

S55066

trypsin (EC 3.4.21.4) II precursor, pancreatic (clone 2-P29) - chicken

N;Alternate names: trypsinogen II

C:Species: Gallus gallus (chicken)

C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 22-Jun-1999

C:Accession: S55066; S72347

R;Wang, K.; Gan, L.; Lee, I.; Hood, L.

Biochem. J. 307, 471-479, 1995

A:Title: Isolation and characterization of the chicken trypsinogen gene family.
 A:Reference number: S55065; MUID:95251611; PMID:7733885

A:Accession: S55066

A:Molecule type: mRNA

A:Residues: 1-248 <WAN1>

A:Cross-references: EMBL:U15157; NID:G603906; PIDN:AAA79914.1; PID:G603907

A:Experimental source: clone 2-P29

A:Accession: S72347

A:Molecule type: DNA

A:Residues: 1-248 <WAN2>

A:Cross-references: EMBL:U15157; NID:G603906; PIDN:AAA79914.1; PID:G603907

A:Experimental source: clone 2-P29

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-25/Domain: activation peptide #status predicted <APT>

F:26-248/Product: trypsin II #status predicted <MAT>

F:26-241/Domain: trypsin homology <TRY>

F:65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.4%; Score 569.5; DB 2; Length 248;

Best Local Similarity 47.5%; Pred. NO. 2.9e-39;

Matches 116; Conservative 39; Mismatches 76; Indels 11; Gaps 6;

Qy 5 LFLILCVLGLS-----QAATPKIFNGTECGNSOPWQVGLPECTSLRCGGVLIDHRVLT 59

Db 4 LFLILCVLGLS-----QAATPKIFNGTECGNSOPWQVGLPECTSLRCGGVLIDHRVLT 59

Qy 60 AAHCSSRYVRLGHEHSLQSDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVR 119

Db 63 AAHCSSRYVRLGHEHSLQSDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLPVR 119

Qy 120 VTSSVQPLPNDCATAGTECHVSGWGTINHPRPFPDQLQCLNLSIVSHATCHGVYVGR 179

Db 121 VSADIQPIALPSSCAKAGTECHVSGWGTINHPRPFPDQLQCLNLSIVSHATCHGVYVGR 179

Qy 180 ITSNVVCAGVP-GQDACQSGSGPLVCGVQLGVLVSGVSGPCQDQGIPIGVYTYICVY 238

Db 181 ITSNVVCAGVP-GQDACQSGSGPLVCGVQLGVLVSGVSGPCQDQGIPIGVYTYICVY 238

Qy 239 DWIR 242

Db 239 DWIQ 242

RESULT 3

S55067

trypsin (EC 3.4.21.4) I precursor, pancreatic - chicken

N:Alternate names: trypsinogen I

C:Species: Gallus gallus (chicken)

C>Date: 28-Oct-1996 #sequence revision 07-Feb-1997 #text_change 21-Jul-2000

C:Accession: S55067; S72345; S55065; S72346; S71155

R:Wang, K.; Gan, L.; Lee, I.; Hood, L.

Biochem. J. 307, 471-479, 1995

A:Title: Isolation and characterization of the chicken trypsinogen gene family.

A:Reference number: S55065; MUID:95251611; PMID:7733885

A:Accession: S55067

A:Molecule type: mRNA

A:Residues: 1-248 <WAN1>

A:Cross-references: EMBL:U15156; NID:G603904

A:Experimental source: clone 1-P38

A:Accession: S72345

A:Molecule type: DNA

A:Residues: 1-248 <WAN2>

A:Experimental source: clone 1-P38

A:Accession: S55065

A:Molecule type: mRNA

A:Residues: 1-9, 'V', 'I', '11-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 <WAN3>

A:Cross-references: EMBL:U15155; NID:G603902; PIDN:AAA79912.1; PID:G603903

A:Experimental source: clone P1

A:Accession: S72346

A:Molecule type: DNA

A:Residues: 1-9, 'V', 'I', '11-12, 'T', '14-102, 'A', '104-214, 'I', '216-248 <WAN4>

A:Cross-references: GB:U15155; NID:G603902; PIDN:AAA79912.1; PID:G603903

A:Experimental source: clone P1

R:Wang, K.

submitted to the EMBL Data Library, September 1994

A:Reference number: S71155

A:Accession: S71155

A:Molecule type: mRNA

A:Residues: 1-102, 'A', '104-248 <WAN5>

A:Cross-references: EMBL:U15156; NID:G603904; PIDN:AAA79913.1; PID:G603905

A:Experimental source: clone 1-P38

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen

F:1-15/Domain: signal sequence #status predicted <SIG>

F:16-25/Domain: activation peptide #status predicted <APT>

F:26-248/Product: trypsin I #status predicted <MAT>

F:26-241/Domain: trypsin homology <TRY>

F:65,109,202/Active site: His, Asp, Ser #status predicted

Query Match 41.3%; Score 567; DB 2; Length 248;

Best Local Similarity 45.5%; Pred. No. 4.6e-39;

Matches 115; Conservative 38; Mismatches 88; Indels 12; Gaps 6;

Qy 3 LSIFLLCVLQ-----LSQAATPKIFNGTECGNSOPWQVGLPEGTSILRCGGVLIDHRW 56

Db 1 MKFVLVAFVAVAPFISDEDDDKIVGGYSCARSAPYQVSLNSGYHF-CGGSLSISQM 59

Qy 57 VLTAAHCSSRYVRLGHEHSLQSDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLRL 116

Db 60 VLSAAHCSSRYVRLGHEHSLQSDWTEQIRHSGFVTHPGYLGASTSHEHDLRLRLRL 116

Qy 117 PVRTSSVQPLPNDCATAGTECHVSGWGTINHPRPFPDQLQCLNLSIVSHATCHGVY 176

Db 118 AATLNSYVNTVPLPTSCVTAGTCLISGWNLTSSGSLYPDVQLCLNAPVLSSSQCSAY 177

Qy 177 PGRITSNVVCAGVP-GQDACQSGSGPLVCGVQLGVLVSGVSGPCQDQGIPIGVYTYIC 235

Db 178 PGRITSNVVCAGVP-GQDACQSGSGPLVCGVQLGVLVSGVSGPCQDQGIPIGVYTYIC 235

Qy 236 KYDWMIRMIMRN 248

Db 236 NYVSWIKTMSN 248

RESULT 4

TRPGTR

trypsin (EC 3.4.21.4) precursor - pig (tentative sequence)

N:Contains: trypsinogen

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A90641; A90368; A00947

R:Charles, M.; Roversy, M.; Guidoni, A.; Desnuelle, P.

Biochim. Biophys. Acta 69, 115-129, 1983

A:Title: Su le trypsinogene et la trypsine de porc.

A:Reference number: A90641

A:Accession: A90641

A:Molecule type: protein

A:Residues: 1-10 <CHA>

R:Hermodeson, M.A.; Ericsson, L.H.; Neurath, H.; Walsh, K.A.

Biochemistry 12, 3146-3153, 1973

A:Title: Determination of the amino acid sequence of porcine trypsin by sequenator anal

A:Reference number: A90368; MUID:73258692; PMID:4738933

A:Accession: A90368

A:Molecule type: protein

A:Residues: 9-231 <HER>

A:Note: at position 20, Ile and Val occur alternatively

C:Superfamily: trypsin; trypsin homology

C:Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase; zym

F:1-231/Product: trypsinogen #status experimental <ZYM>

F:1-8/Domain: activation peptide #status experimental <APT>

F:9-231/Product: trypsin #status experimental <MAT>

F:9-224/Domain: trypsin homology <TRY>

F:15-145, 33-49, 117-218, 124-191, 156-170, 181-205/Disulfide bonds: #status predicted

F:48, 92, 185/Active site: His, Asp, Ser #status predicted

```

F;60,62,65,70/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
Query Match      40.8%; Score 561; DB 1; Length 231;
Best Local Similarity 46.7%; Pred. No. 1.3e-38;
Matches 107; Conservative 39; Mismatches 77; Indels 6; Gaps 4;

Qy 21 KIFNGTEGCRNSQWQVGLPFGTSLRCGGVLIDHRWLVTAAHCSSGYWVRLGHSLSQL 80
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 8 KIVGGYCAANSIPYQVSLNCSGSHF-CGGSLLNSGWVWSAAHCYKRSIQVRLGSEHNDVL 66
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 81 DWTEQIRHSGFSVTHPGVIGASTSHEHDLRLRLRLPVRVTSSVQPLPLPNDCATATGEC 140
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 EGNEQFINAAKIIITHPFNG--NTLDDNDIMLIKSSPATLNSRVATVSLPRSCAAAGTEC 124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 141 HVSWGIGITNHPNRPFPDLLOCLNLSIVSHATCHGVYFGRITSNVNCAGGVP-GQDACQGD 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 LISGKNTKSSGSSVPSLQCLKAPVLSDDSSCKSSYPQQTGNMICVGPLBGGKDSQCGD 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 200 SGGPLVCGGVLOGLVWSGVSQCGDGPVGVYTYICKYVDWIRMIMRNN 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 SGGPVCVNGQLGVISWGY--GCAQKPKGVYTKVCNVVNNIQOTIAAN 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
A35871
trypsin (EC 3.4.21.4) precursor, pancreatic - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 04-Mar-2000
C:Accession: A35871; S12117
R:Shi, Y.B.; Brown, D.D.
Genes Dev. 4, 1107-1113, 1990
A:Title: Developmental and thyroid hormone-dependent regulation of pancreatic
A:Reference number: A35871; MUID:91007255; PMID:2210372
A:Accession: A35871
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-243 <SH1>
A:Cross-references: EMBL:X53458; NID:G65162; PIDN:CAA37538.1; PID:G65163
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; protein digestion; serine proteinase
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-20/Domain: activation peptide #status predicted <APT>
F:21-236/Domain: trypsin homology <TRY>
F:26-243/Product: trypsin I #status predicted <NAT>
F:27-157,45-61,129-230,136-203,168-182/Disulfide bonds: #status predicted
F:60,104,197/Active site: His, Asp, Ser #status predicted

Query Match      40.4%; Score 555; DB 2; Length 243;
Best Local Similarity 45.7%; Pred. No. 4.3e-38;
Matches 113; Conservative 42; Mismatches 82; Indels 10; Gaps 6;

Qy 6 PLLLCVLGLSQAAT--PKIFNGTEGCRNSQWQVGLPFGTSLRCGGVLIDHRWLVTAAH 62
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 PLLLCVL-LGMAAFDDDKIGGATCAKSSYPYIVLSNNGHFP-CGGSLLTNQWWSAAH 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 63 CSGRYVWVRLGHSLSQDWTQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTS 122
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 CYKASIQVRLGHEHIALSEGTQFISSKVRHSGY--NSYTLDDNDIMLIKSSPASLNA 118
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 123 SVQPLPLPNDCATATGTECHVSGWGITNHPNRPFPDLLOCLNLSIVSHATCHGVYFGRITS 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 119 AVNTVPLPFGCSAAAGTSLISGWGNTLSNGSNYPDLLQCLNAPILITNAQCNSAYPGRITA 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 183 NWCAGGVP-GQDACQGDGSLPVCVGLVOCGLVWSGVSQCGDGIIPGVYTYICKYVDWI 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 179 NMICVGYMEGKDSQCGDSGFPVVCNGQLQGVWSWGY--GCAMRNPFGVYTKVCYNNAWI 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 242 RMIMRNN 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 QNTIAAN 243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6

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A53968
serine proteinase SCCE precursor - human
N:Alternate names: stratum corneum chymotryptic enzyme
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 22-Jun-1999
C:Accession: A53968
R:Hansson, L.; Stromqvist, M.; Baekman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A:Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A:Reference number: A53968; MUID:94308225; PMID:8034709
A:Accession: A53968
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-253 <HAN>
A:Cross-references: GB:L33404; NID:9521214; PIDN:AAC37551.1; PID:G532504
C:Genetics:
A:Gene: GDB:PRSS6; SCCE
A:Cross-references: GDB:377730
A:Map position: 7q35-7q35
C:Superfamily: trypsin; trypsin homology
P:30-245/Domain: trypsin homology <TRY>

Query Match 40.4%; Score 555; DB 2; Length 253;
Best Local Similarity 44.7%; Pred. No. 4.5e-38;
Matches 115; Conservative 37; Mismatches 90; Indels 16; Gaps 6;

Qy 1 MGLSIFLLLCVLGLS-----QAATPKIFNGTECRNSQPMQVGLPEGTSLRGGVLI 52
Db 1 MARSLPLQLILLSLALETAGEAQQDKIIDGAPCARGSHPMQVALLSGNQLHCGVLV 60

Qy 53 DHRVLTAAHCGSGSYVRLGHEHSLSQDWTQIRHSGFVTHPGYLGASTSHEHDLRL 112
Db 61 NERVLTAAHCKMNEYTVHLGSDTLG--DRAQRIRAKSKSFRHFGY--STQTHVNDLMLV 116

Qy 113 RLRLPVRVTSSVQPLPLNDCTAGTCVHSGHGITHNPRNPDDLQCLNLSIVSHATC 172
Db 117 KLSQARLSNMVKVRLPRSCBPPTCTVSGMGTTSPDVPFSDLMCVDKLISPDQC 176

Qy 173 HGVYPRGRTSNMVCAGVPG--QDACQSGSGPLVCGVGLQGLVSGSVGPGQGDGIPGV 230
Db 177 TKVYKDLLENMLCA-GTPDSKKNACGSGGGLVCRGTQLGLVSWGTF-PCGQPNPDGV 234

Qy 231 YTYICKYVDVIRMTIRNN 248
Db 235 YTVQCKPTKINDTMKKH 252

RESULT 7
B25528
trypsin (EC 3.4.21.4) precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 22-Jun-1999
C:Accession: B25528
R:Stevenson, B.J.; Hagenbuechle, O.; Wellauer, P.K.
Nucleic Acids Res. 14, 8307-8330, 1986
A:Title: Sequence organisation and transcriptional regulation of the mouse elastase II
A:Reference number: A93646; MUID:87066713; PMID:3641189
A:Accession: B25528
A:Molecule type: mRNA
A:Residues: 1-246 <STB>
A:Cross-references: GB:X04574; NID:954918; PIDN:CAA28243.1; PID:G54919
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase
P:1-23/Domain: signal sequence #status predicted <SIG>
P:24-246/Product: trypsin #status predicted <MAT>
P:24-239/Domain: trypsin homology <TRY>
P:30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
P:63,107,200/Active site: His, Asp, Ser #status predicted
P:75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 40.2%; Score 553; DB 2; Length 246;
Best Local Similarity 44.7%; Pred. No. 6.3e-38;
Matches 113; Conservative 45; Mismatches 81; Indels 14; Gaps 7;

A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
R:MacDonald, R.J.; Scary, S.J.; Swift, G.H.
J. Biol. Chem. 257, 9724-9732, 1982
A:Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of
A:Reference number: A00948; MUID:82265624; PMID:6896710
A:Accession: A00948
A:Molecule type: mRNA
A:Residues: 1-246 <MAC>
A:Cross-references: GB:J00778; NID:g206507; PIDN:AAA98518.1; PID:g206508
C:Genetics:
A:Introns: 14/1; 67/2; 152/1; 197/3
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-246/Product: trypsin I #status predicted <ENZ>
F:24-239/Domain: trypsin homology <TRY>
F:30-160, 48-64, 132-233, 139-206, 171-185/Disulfide bonds: #status predicted
F:63, 107, 200/Active site: His, Asp, Ser #status predicted
F:75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 39.5%; Score 543; DB 1; Length 246;
Best Local Similarity 44.5%; Pred. No. 4.1e-37;
Matches 110; Conservative 47; Mismatches 76; Indels 14; Gaps 7;

Qy 3 LSIFLLCVLGLSQA----ATPKIFNGTTCGRNSQPMQVGLFEGTSLRCGGVLIDHRWVL 58
Db 1 MSALLILALGAVAFLPEDDDKIVGGYTCPEHSVPYQVLSNGVHF-CGGSLINDQWV 59

Qy 59 TAAHCSGRYVWRLGHEHSLDQWTEQIRHSGFSVTHPGVGLGASTSHEHDLRLRLPV 118
Db 60 SAAHCYSRIQVRLGHEHNLVLEGGQETNAKIKHPNY--SSKTLNDIMLKLSQSPV 117

Qy 119 RVTSSVQPLPNDCAATGTECHVSGMG--ITNHPNPFPDLLQCLNLSIVSHATCHGVY 176
Db 118 KLNARVAPALPSACAPAGTQCLISGNGTSLNGVNN--PDLLQCVADPVLQADCAAY 175

Qy 177 PGRITSNMVCAGVP-GQDACQDGGPLVCGVGLQGLVSGVSGPCQDGIPIGVYVIC 235
Db 176 PGEITSSMICVGFLEGGKDSQCGSGGPPVCGVGLQGLVSGVY--GCALPDNPVGYTKVC 233

Qy 236 KYVDWIR 242
Db 234 NFVGWIQ 240

RESULT 14
S31779
trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C:Species: Salmo salar (Atlantic salmon)
C:Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C:Accession: S66657; S31779
R:Male, R.; Lorenz, J.B.; Snalaa, A.O.; Torriessen, K.R.
Eur. J. Biochem. 232, 677-685, 1995
A:Title: Molecular cloning and characterization of anionic and cationic variants of try
A:Reference number: S66657; MUID:96035908; PMID:7556223
A:Accession: S66657
A:Molecule type: mRNA
A:Residues: 1-238 <MAL>
A:Cross-references: EMBL:X70074; NID:g64387; PIDN:CAA49679.1; PID:g64388
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine proteinase
F:1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F:8-15/Domain: activation peptide #status predicted <APT>
F:16-238/Product: trypsin III #status predicted <MAT>
F:16-231/Domain: trypsin homology <TRY>
F:22-152, 40-56, 124-225, 131-198, 163-177, 188-212/disulfide bonds: #status predicted
F:55, 99, 192/Active site: His, Asp, Ser #status predicted

Query Match 39.3%; Score 540; DB 2; Length 238;
Best Local Similarity 47.2%; Pred. No. 7e-37;
Matches 108; Conservative 37; Mismatches 78; Indels 6; Gaps 4;

Qy 21 KIFNGTTCGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLTAHCSGRYVWRLGHEHSL 80
Db 15 KIVGGYECRKNSASYQASLQSGYHF-CGSLISSITWVYVSAACHYKSRIOVRLGEHNI 73

Qy 81 DWTEQIRHSGFSVTHPGVGLGASTSHEHDLRLRLPVRTVSSVQPLPNDCAATGTEC 140
Db 74 EGTEQFIDSVKVINHPSY--NSRNDINDIMLIKSPASLNSYVSTVALPSSCASSGTTC 131

Qy 141 HVSGMGITNHPNPFPDLLQCLNLSIVSHATCHGVYPIGVYVICVVDWIRIMRN 248
Db 132 LVSCMGNLSSGSSNYPDTLRCLDLPILSSSCNSAYPGQITSNMPCAFMEGGKDSQCGD 191

Qy 200 SGGPLVCGVGLQGLVSGVSGPCQDGIPIGVYVICVVDWIRIMRN 248
Db 192 SGGPWCNQLQGVVSWGY--GCAQRNKPQVYTKVYRYSWISMTSSN 238

RESULT 15
S05494
trypsin (EC 3.4.21.4) IV precursor - rat
N:Alternate names: 23K protein; trypsinogen IV precursor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
C:Accession: S05494
R:Luettcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989
A:Title: A fourth trypsinogen (p23) in the rat pancreas induced by CCK.
A:Reference number: S05494; MUID:89386010; PMID:2780302
A:Accession: S05494
A:Molecule type: mRNA
A:Residues: 1-247 <LUB>
A:Cross-references: EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814
C:Superfamily: trypsin; trypsin homology
C:Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-23/Domain: activation peptide #status predicted <APT>
F:24-247/Product: trypsin IV #status predicted <MAT>
F:24-240/Domain: trypsin homology <TRY>
F:30-161, 49-65, 133-234, 140-207, 172-186/Disulfide bonds: #status predicted
F:64, 108, 201/Active site: His, Asp, Ser #status predicted
F:76, 78, 81, 86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted

Query Match 38.8%; Score 533.5; DB 2; Length 247;
Best Local Similarity 43.4%; Pred. No. 2.5e-36;
Matches 109; Conservative 41; Mismatches 94; Indels 7; Gaps 4;

Qy 1 MGLSIF--LLLCVLGLSQAATPKIFNGTTCGRNSQPMQVGLFEGTSLRCGGVLIDHRWVL 58
Db 1 MKISIFAFPLGAVALPVDNDKIVGGYTCPKHLVPYQVSLHDGISHQCGGSLISQWVL 60

Qy 59 TAAHCSGRYVWRLGHEHSLQLOWTEQIRHSGFSVTHPGVGLGASTSHEHDLRLRLPV 118
Db 61 SAAHCYKRLQVRLGHEHNLVLEGGQETDAEKIRHPEY--NKDTLNDIMLIKLSQSPA 118

Qy 119 RVTSSVQPLPNDCAATGTECHVSGHGTNHPNPFPDLLQCLNLSIVSHATCHGVY 178
Db 119 VLNSQVSTVSLPFRSCASTDAQCLVSGMGNTVISGKTPALLQCLEAPVLSSACKSKSPG 178

Qy 179 RITSNMVCAGVP-GQDACQDGGPLVCGVGLQGLVSGVSGPCQDGIPIGVYVIC 237
Db 179 QITSNMFCFLFLEGGKDSQCGSGPVCNGEIGIVSGSV--CAMRGKGVYTKVCNY 236

Qy 238 VDWIRIMRN 248
Db 237 LSWIQETMANN 247

Search completed: June 16, 2004, 15:06:51
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 14:58:55 ; Search time 17 Seconds
(without alignments)
759.612 Million cell updates/sec

Title: US-10-006-116A-194
Perfect score: 1374
Sequence: 1 MGLSIFLLLCVLGLSQAATP.....GVYTYICKYVDWIRMIKRN 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1374	100.0	248	1	KLK8_HUMAN
2	630.5	45.9	260	1	KLK8_HUMAN
3	622.5	45.3	260	1	NRPN_MOUSE
4	621.5	45.2	260	1	NRPN_RAT
5	618.5	45.0	250	1	KLK8_HUMAN
6	599	43.6	256	1	KLK8_HUMAN
7	569.5	41.4	248	1	TRY3_CHICK
8	569.5	41.4	251	1	KLK8_HUMAN
9	568.5	41.4	250	1	KLK8_HUMAN
10	567	41.3	277	1	KLK8_HUMAN
11	566	41.2	248	1	TRY2_CHICK
12	565	41.1	248	1	TRY1_CHICK
13	564.5	41.1	293	1	KLK5_HUMAN
14	564	41.0	276	1	KLK8_HUMAN
15	563	41.0	244	1	TRY2_XENLA
16	561	40.8	231	1	TRY1_PIG
17	561	40.8	243	1	TRY1_BOVIN
18	561	40.8	244	1	KLK6_HUMAN
19	555	40.4	243	1	TRY1_XENLA
20	555	40.4	253	1	KLK7_HUMAN
21	553	40.2	246	1	TRY2_MOUSE
22	550	40.0	247	1	TRY2_BOVIN
23	546	39.7	247	1	TRY2_CANFA
24	545	39.7	246	1	TRY1_CANFA
25	544.5	39.6	247	1	TRY1_RAT
26	543	39.5	246	1	TRY1_RAT
27	540	39.3	238	1	TRY3_SALSA
28	533.5	38.8	247	1	TRY4_RAT
29	533	38.8	246	1	TRY2_RAT
30	527.5	38.4	261	1	KLK7_RAT
31	521.5	38.0	246	1	KLK_PIG
32	521.5	38.0	261	1	KLK6_MOUSE
33	519	37.8	246	1	TRY4_RAT

34	518	37.7	246	1	TRYB_RAT
35	518	37.7	261	1	KLK8_RAT
36	513.5	37.4	231	1	TRY2_SALSA
37	513.5	37.4	239	1	KLK3_MOUSE
38	510.5	37.2	261	1	KLK3_MOUSE
39	508	37.0	242	1	TRY1_SALSA
40	505	36.8	260	1	EST1_CANFA
41	503	36.6	263	1	KLK8_PRANA
42	502	36.5	259	1	KLK8_RAT
43	501	36.5	247	1	TRY2_HUMAN
44	499.5	36.4	241	1	TRYX_GADMO
45	498	36.2	254	1	KLK4_HUMAN

ALIGNMENTS

RESULT 1	KLK8_HUMAN	STANDARD;	PRT;	248 AA.
AC	Q9UKR0; Q9UKR1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5) (KLK-L5).			
GN	KLK12 OR KLK15.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20118156; PubMed=10652563;			
RA	Youssef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4".			
RT	19q13.3-q13.4".			
RL	Anticancer Res. 19:2843-2852(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Youssef G.M., Magklara A., Scorilas A., Diamandis E.P.;			
RT	"Cloning of new alternatively spliced forms of the kallikrein-like gene 5 (KLK-L5)".			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paepker B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."			
RL	Gene 257:119-130(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala M., Terry A., Brower A., Ganes J., Danganan L., Eriar A., Christensen M., Georgescu A., Avila J., Liu S., Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;			
RT	"Sequence analysis of chromosome 19q13.4".			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
CC	-I- SUBCELLULAR LOCATION: Secreted (Probable).			
CC	-I- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	isoId=Q9UKR0-1; Sequence=Displayed;			
CC	Name=2;			
CC	isoId=Q9UKR0-2; Sequence=VSP_005403;			
CC	-I- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.			

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DR EMBL; AF135025; AAD26426.2; -;
 DR EMBL; AF135025; AAF06065.1; -;
 DR EMBL; AF241327; AAG33365.1; -;
 DR EMBL; AC011473; AAG23258.1; -;
 DR HSSP; P00763; IDPO.
 DR MEROPS; S01.020; -;
 DR Genew; HGNC:6360; KLIK12.
 DR MIM; 605539; -;
 DR GO; GO:000576; C:extracellular; NAS.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Cys Ser. trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydrolase; Serine protease; Glycoprotein; Signal;
 KW Alternative splicing.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 248 KALLIKREIN 12.
 FT ACT_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 28 161 BY SIMILARITY.
 FT DISULFID 47 63 BY SIMILARITY.
 FT DISULFID 133 235 BY SIMILARITY.
 FT DISULFID 140 206 BY SIMILARITY.
 FT DISULFID 172 186 BY SIMILARITY.
 FT DISULFID 196 222 BY SIMILARITY.
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 236 248 KYVDVIRIMRN -> NSTLVGLGTSWNFSQPF (in
 FT isoform 2).
 FT /FTID=VSP 005403.
 SQ SEQUENCE 248 AA; 26733 MW; BB473B8FBFAF703 CRC64;

Query Match 100.0%; Score 1374; DB 1; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.7e-105;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSIFLLCVGLSQAAATPKIFNTECGRNSQPMQVGLFECTSLRCGVLIDHRWVLA 60
 DB 1 MGLSIFLLCVGLSQAAATPKIFNTECGRNSQPMQVGLFECTSLRCGVLIDHRWVLA 60
 QY 61 AHCSSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 DB 61 AHCSSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDCATAGTECHVSGWGIHTNPRNPFDLLQCLNLSIVSHATCHGVYPCR 180
 DB 121 TSSVQPLPLPNDCATAGTECHVSGWGIHTNPRNPFDLLQCLNLSIVSHATCHGVYPCR 180
 QY 181 TSNMVCAGVPQDAGCGSGPLVCGVQLGVLSWGSVPGCGDIPGVYTYCKYVDW 240
 DB 181 TSNMVCAGVPQDAGCGSGPLVCGVQLGVLSWGSVPGCGDIPGVYTYCKYVDW 240
 QY 241 IRIMIRN 248
 DB 241 IRIMIRN 248

RESULT 2
 KLIK HUMAN STANDARD; PRT; 260 AA.
 ID KLIK_HUMAN O60259; O9HCB3; O9U47; 260 AA.
 AC O60259; O9HCB3; O9U47; 260 AA.
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neuropain precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Ovasin) (Serine
 DE protease TADG-14) (tumor-associated differentially expressed gene-14
 DE protein).
 GN KLIK OR PRSS19 OR TADG14 OR NRPN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE-Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neuropain cDNA and gene.";
 RL Gene 213:9-16(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=99203457; PubMed=10102990;
 RA Mitani S., Teurloka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neuropain, a brain-related serine protease, is
 RT generated by alternative splicing and is expressed preferentially in
 RT human adult brain";
 RL Eur. J. Biochem. 260:627-634(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
 RA O'Brien T.J.;
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel
 RT serine protease overexpressed by ovarian carcinoma.";
 RL Cancer Res. 59:4435-4439(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;
 RT "Molecular cloning and characterization of a novel serine protease,
 RT ovasin, a potential molecular marker for ovarian carcinomas.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20510030; PubMed=11054574;
 RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McQuig J.,
 RA Moss P., Paepker B., Wang K.;
 RT "Sequencing and expression analysis of the serine protease gene
 RT cluster located in chromosome 19q13 region.";
 RL Gene 257:119-130(2000).
 RN [6]
 RP SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
 RA Phan H., Velasco N., Do L., Regala M., Terry A., Brower A., Ganes J.,
 RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;

RT plasticity-related serine protease.";
 RL J. Biol. Chem. 273:11189-11196(1998).
 [5]
 RN X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
 RC TISSUE=Hippocampus;
 RX MEDLINE=99134351; PubMed=9933620;
 RA Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
 RA Shiosaka S., Hakoshima T.;
 RT "Crystal structure of neuropsin, a hippocampal protease involved in
 RT kindling epileptogenesis.";
 RL J. Biol. Chem. 274:4220-4224(1999).
 CC -!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
 CC hippocampal plasticity. Has a strong proteolytic activity against
 CC fibronectin.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
 CC -!- ENZYME REGULATION: Strongly inhibited by diisopropyl
 CC fluorophosphate, leupeptin and (4-aminophenyl)methanesulfonyl 1-
 CC fluoride.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of
 CC mouse brain and is localized at highest concentration in pyramidal
 CC neurons of the hippocampal CA1-3 subfields.
 CC -!- MASS SPECTROMETRY: MW=26613; METHOD=MALDI; RANGB=29-260.
 CC -!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGB=33-260.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.

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 DR EMBL; D30785; BAA06451.1; -;
 DR EMBL; AB032202; BAA92435.1; -;
 DR EMBL; BC055895; AAH55895.1; -;
 DR PIR; I56559; I56559.
 DR PDB; INPM; 2J-MAR-99.
 DR MEROPS; S01.244; -;
 DR MGD; MGI:892018; K1K8.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp SPC; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;
 FT 3D-structure.
 FT SIGNAL 1 28 POTENTIAL.
 FT PROPEP 29 32
 FT CHAIN 33 260
 FT ACT_SITE 73 73
 FT ACT_SITE 120 120
 FT ACT_SITE 212 212
 FT DISULFID 39 173
 FT DISULFID 58 74
 FT DISULFID 145 246
 FT DISULFID 152 218
 FT DISULFID 184 198
 FT DISULFID 208 233
 FT CARBOHYD 110 110
 FT STRAND 34 34
 FT STRAND 37 38
 FT TURN 41 42
 FT TURN 45 46
 FT STRAND 47 52
 FT TURN 53 54
 FT STRAND 55 64
 FT TURN 65 66
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT STRAND 67 70
 FT HELIX 72 74
 FT STRAND 80 83
 FT STRAND 87 87
 FT TURN 88 89
 FT STRAND 96 98
 FT STRAND 100 105
 FT TURN 107 108
 FT TURN 114 115
 FT TURN 118 119
 FT TURN 122 126
 FT STRAND 140 141
 FT TURN 148 149
 FT STRAND 151 156
 FT STRAND 170 170
 FT STRAND 172 178
 FT HELIX 181 187
 FT TURN 189 191
 FT TURN 194 195
 FT STRAND 196 200
 FT TURN 202 203
 FT STRAND 206 206
 FT TURN 209 210
 FT TURN 212 213
 FT STRAND 215 218
 FT TURN 219 220
 FT STRAND 221 228
 FT STRAND 235 235
 FT TURN 236 237
 FT STRAND 238 238
 FT STRAND 240 244
 FT HELIX 245 256
 SQ SEQUENCE 260 AA; 28523 MW; BE5F6F6BE37CD60E CRC64;
 Query Match 45.3%; Score 622.5; DB 1; Length 260;
 Best Local Similarity 49.0%; Pred. No. 5.1e-44;
 Matches 121; Conservative 28; Mismatches 93; Indels 5; Gaps 3;
 Oy 5 IFLLLCV---LGLSQAATPKIFNTECGRNSQPMQVGLFEGTSLRCCGVLDHRRVLTAA 61
 Db 13 ILLLLPFGAWAGLTRAQCSKILEGRCITPHSQPQAALFQGERLTCGGVLVGDRLVLTAA 72
 Oy 62 HCSGRYVRLGHEHLSQLDWTQEI RHSGFSVTHPGVLGAS-TSEHDLRLRLRPVRV 120
 Db 73 HCKQKYSVRLGSHSLQSRDQPEQEIQVAQSIQPCYNNSPEDSHDMLRLQNSAL 132
 Oy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDILLOCLNLSIVSHATCHGYYPGR 180
 Db 133 GDKVPVQLANLCPKVGOKCIISGWTVPQENFPNTLNCAEVKIYSONKCEAYPGKI 192
 Oy 181 TSNMVCAGGVPGQDACQGDGSGPLVCGGVLCGLVSGVSGVCGQDGIPIGVYICKYVDW 240
 Db 193 TEGMVCAGSSNGADTCQDGSGLVCDMLQGITSWGSD-DFCGKPEKPGVVTIKICRYTTW 251
 Oy 241 IRMLMRN 247
 Db 252 IKKTMDN 258
 RESULT 4
 NRPN RAT
 ID NRPN RAT STANDARD; PRT; 260 AA.
 AC O88780;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropain precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
 DE protease 1).
 GN K1K8 OR PRSS19 OR NRPN OR BSPI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.
RC STRAIN=Fischer; TISSUE=Brain;
RA MEDLINE=98389725; PubMed=9722524;
RX Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;
RT "Serine proteases in rodent hippocampus.";
RL J. Biol. Chem. 273:23004-23011(1998).
CC -1- FUNCTION: Suggested to be involved in kindling epileptogenesis and
CC hippocampal plasticity. Has a strong proteolytic activity against
CC fibronectin (By similarity).
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: Restricted to hippocampus.
CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC
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CC
CC EMBL: AJ005641; CRA06643.1; -.
CC HSP: Q61955; INPM.
DR MEROPS: S01.244; -.
DR InterPro: IPR009003; Cys_Ser_trypsin.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal.
FT SIGNAL 1 28
FT PROPEP 29 32
FT CHAIN 33 260
FT ACT_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 39 173 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 145 246 BY SIMILARITY.
FT DISULFID 152 218 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 260 AA; 28510 MW; 58DF4F0602A0B7F5 CRC64;

Query Match 45.2%; Score 621.5; DB 1; Length 260;
Best Local Similarity 48.6%; Pred. No. 6.1e-44;
Matches 118; Conservative 32; Mismatches 90; Indels 3; Gaps 3;

QY 5 IFLL-CVTLGSOATPKIPNGTECCRNQSPQVGLPFGTSLRCGGVLIDHRWLTAAHC 63
DB LFLLMGAWAGLTRAQGSKILEGQECXPHSQPWQTAALFQGERLVCCGVLGDRWLTAAHC 74
QY 64 SGRYVVRLEHSLQLDWTEQIRHSGFSVTHPGYLGA-TSHEDRLRLRLPVRVTS 122
DB KDKYSVRLGDHSLQKRDEPEIQVARSIQHPFCFNSSPEDHSDIMLIRLQNSANLGD 134
QY 123 SVQPLPLPNDCATAGTECHVSGWGNTNHPNPPFDLLQLCLNLISVSHATCHGVYPGRTS 182
DB KVKPIELANLCPKVGQKCIISGWGTVTSPOENFTNLCAEVKIYQNKCRAYPKITE 194
QY 183 NMVCAGVPEQDAQCGDSGGLVCGGVQLVSGVSGPGQDGIPGVYTYICKYVDWIR 242
DB GMYCAGSSNGADTCQDSGGLVCGGVQLVSGVSGPGQDGIPGVYTYICKYVDWIR 253
QY 243 MIM 245

Db 254 KTM 256
RESULT 5
KLKB HUMAN STANDARD; PRT; 250 AA.
AC Q9UBX7; O75837; Q9NS65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like
DE protease).
GN KLK11 OR PRSS20 OR TLSP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Hippocampus;
RX MEDLINE=98438738; PubMed=9765601;
RA Yoshida S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
RT "cDNA cloning and expression of a novel serine protease, TLSP.";
RL Biochim. Biophys. Acta 1199:225-228(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Hippocampus, and Prostate;
RX MEDLINE=20329229; PubMed=10872828;
RA Mitani S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;
RT "A novel isoform of a kallikrein-like protease, TLSP/hippostasin,
RT (PRSS20), is expressed in the human brain and prostate.";
RL Biochem. Biophys. Res. Commun. 272:205-211(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20130117; PubMed=10662548;
RA Yousef G.M., Scorilas A., Diamandis E.P.;
RT "Genomic organization, mapping, tissue expression, and hormonal
RT regulation of trypsin-like serine protease (TLSP PRSS20), a new
RT member of the human kallikrein gene family.";
RL Genomics 63:88-96(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RA Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
RA Dangnan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carraro A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

FT DISULFID 134 235 BY SIMILARITY.
 FT DISULFID 141 208 BY SIMILARITY.
 FT DISULFID 173 187 BY SIMILARITY.
 FT DISULFID 198 222 BY SIMILARITY.
 FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
 SQ SEQUENCE 248 AA; 26622 MW; E516B07622B588E CRC64;
 Query Match 41.4%; Score 569.5; DB 1; Length 248;
 Best Local Similarity 47.5%; Pred. No. 1e-39;
 Matches 116; Conservative 39; Mismatches 78; Indels 11; Gaps 6;
 QY 5 IFLLCVLGLS-----QAATPKIFNGTEGGRNSQPMQVGLFECTSLR--CGGVLIDHR 59
 DB 4 LFLILSCIGAAVAFPGGADDDKIVGCTCPKPSVYQVSLNSGYHF-CGGLSLNSQWVLS 62
 QY 60 AAKHSGSYWVRLGHSLSQLDWTQIRHSGSVTHPGVLGASTSHEHDLRLRLRPLVR 119
 DB 63 AAKCYKSRIQVRLGHEYNIDVEDSEVRSSVIRHPKY--SSITLNDIMLIKLASAVE 120
 QY 120 VTSSVQPLPLPNDCATAGTECHVSGMGITNHPNPPDLLQCLNLSIVSHATCHGVYGR 179
 DB 121 YSADIQIPLPSCAKAGTECLISGWNTLSNGYNPELLQCLNAPILSDQECQAYPGD 180
 QY 180 ITSNMVCAGVP-GQDACQDSGGPLVCGGVGLVSGSVGPCQDGIPIGVYTIKVV 238
 DB 181 ITSNMVCVGFLEGGKSCQDSGGPWCNGELQGVISWG-IG-CALKGYPGVYTKVCNV 238
 QY 239 DWIR 242
 DB 239 DWIQ 242

RESULT 8

KLKE HUMAN
 ID_KLKE HUMAN STANDARD; PRT; 251 AA.
 AC Q9PGG3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6) (KLK-L6).
 DE KLK14 OR KLK6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]_SEQUENCE FROM N.A.
 RA Yousef G.M., Diamandis E.P.;
 RT "Molecular characterization, mapping, and tissue expression of KLK16, a hormonally regulated kallikrein-like gene."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RX MEDLINE=21250997; PubMed=11352573;
 RA Hooper J.D., Bui L.T., Rae F.K., Harvey T.J., Myers S.A.,
 RT Ashworth L.K., Clements J.A.;
 RT "Identification and characterization of KLK14, a novel kallikrein serine protease gene located on human chromosome 19q13.4 and expressed in prostate and skeletal muscle."
 RL Genomics 73:117-122(2001).
 RN [3]
 RA SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
 RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
 RA Danganan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
 RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of chromosome 19q13.4."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

RNA TISSUE SPECIFICITY.
 RX MEDLINE=20545474; PubMed=10969073;
 RA Harvey T.J., Hooper J.D., Myers S.A., Stephenson S.A., Ashworth L.K.,
 RA Clements J.A.;
 RT "Tissue-specific expression patterns and fine mapping of the human kallikrein (KLK) locus on proximal 19q13.4."
 RL J. Biol. Chem. 275:37397-37406(2000).
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- TISSUE SPECIFICITY: High expression in brain, bone marrow and fetal liver. Also expressed in liver, pancreas, fetal spleen, prostate and skeletal muscle.
 CC -1- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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 DR EMBL; AF161221; AAD50773.2; -
 DR EMBL; AF283659; AAK48523.1; -
 DR EMBL; AF283670; AAK48524.1; -
 DR EMBL; AC011473; AAG23260.1; -
 DR HSRP; P00763; IDPO.
 DR MEROPS; S01.029; -
 DR Genew; HGNC:6362; KLK14.
 DR MIM; 606135; -
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal; Zymogen.
 FT SIGNAL 1 18 POTENTIAL.
 FT PROPEP 19 24 ACTIVATION PEPTIDE (POTENTIAL).
 FT CHAIN 25 251 KALLIKREIN 14.
 FT ACT_SITE 67 67 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 111 111 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 204 204 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 31 164 BY SIMILARITY.
 FT DISULFID 52 68 BY SIMILARITY.
 FT DISULFID 143 210 BY SIMILARITY.
 FT DISULFID 175 189 BY SIMILARITY.
 FT DISULFID 200 225 BY SIMILARITY.
 SQ SEQUENCE 251 AA; 27452 MW; 9087953BAPA7ED25 CRC64;
 Query Match 41.4%; Score 569.5; DB 1; Length 251;
 Best Local Similarity 46.9%; Pred. No. 1.e-39;
 Matches 119; Conservative 33; Mismatches 87; Indels 15; Gaps 6;
 QY 5 IFLLCVLGLS-----QAATPKIFNGTEGGRNSQPMQVGLFECTSLR--CGGVLIDHR 55
 DB 1 MFLTLALQVLAIAANTOSQDENKNIIGTCTTRSSQPMQAALLAGPRFLCGALLSQ 60
 QY 56 WLVTAACHSGSRVYVRLGHSLSQLDWTQIRHSGSVTHPGVLGASTSHEHDLRLRLR 115
 DB 61 WVTFAACHGRPIQLVALGKHLRWEATQQVLRVVRQVTHPNY--NSRTHDNDMLQLQ 118
 QY 116 LPVVTSSVQPLPLPNDCATAGTECHVSGMGITNHPNPPDLLQCLNLSIVSHATCHGV 175
 DB 119 QPARIGRAVRPIEVTQACASPCTS CRVSGMGITISSPIARYPASLQCVNINISPDVCQA 178
 QY 176 YPGRITSNMVCAGVP--GQDACQDSGGPLVCGGVGLVSGSVGPCQDGIPIGVYTY 233

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Db 179 YPRTITFGMCA-GVPGGKDSQGGPLVCRGLQGLVSWG-MERCALPGPYGVTN 236
Qy 234 ICKYVDWIRMN 247
Db 237 LCKRSWIETMRD 250

RESULT 9
KLK9 HUMAN
ID_KLK9 HUMAN STANDARD; PRT; 250 AA.
AC Q9UKQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
L3).
GN KLK9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20118156; PubMed=10652563;
RY Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
RT 19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20247258; PubMed=10783266;
RY Yousef G.M., Diamandis E.P.;
RT "The expanded human kallikrein gene family: locus characterization and
RT molecular cloning of a new member, KLK-L3.";
RL Genomics 65:184-194(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510030; PubMed=11054574;
RY Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McQuaig J.,
RY Moss P., Paepel B., Wang K.;
RT "Sequencing and expression analysis of the serine protease gene
RT cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A.
RY Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RY Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RY Phan H., Velasco N., Do L., Regala M., Terry A., Brower A., Garnes J.,
RY Danganan L., Eriar A., Christensen M., Georgescu A., Avila J., Liu S.,
RY Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
RY Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RY Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RY Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal
CC cord.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC
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CC
CC EMBL; AF135026; AAD26427.2; -
CC EMBL; AF243527; AAG33362.1; -
CC EMBL; AC011473; AAG23255.1; -
CC HSSP; P00763; 1DFO.
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DR MEROPS; S01.307; -
DR Genew; HGNC:6370; KLK9.
DR MIM; 605504; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0004252; P:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 15
FT CHAIN 16 250
FT ACT_SITE 63 63
FT ACT_SITE 111 111
FT ACT_SITE 204 204
FT DISULFID 29 164
FT DISULFID 48 64
FT DISULFID 136 238
FT DISULFID 143 210
FT DISULFID 175 189
FT DISULFID 200 225
FT CARBOHYD 131 131
FT CARBOHYD 166 166
FT CARBOHYD 211 211
SQ SEQUENCE 250 AA; 27512 MW; F2785245B063E98B CRC64;

Query Match 41.4%; Score 568.5; DB 1; Length 250;
Best Local Similarity 46.7%; Pred. No. 1.3e-39;
Matches 119; Conservative 32; Mismatches 89; Indels 15; Gaps 7;

Qy 1 MGLSIFLLCVLGLSQATPKI FNGTCGRNSQWQVGLFGTSLRCGVLIDHWLTA 60
Db 3 LGLLCALLSLAGHGWDAT-RAIGAEBCRPNSQWQVGLFHLTRFCGATLISDRWLLTA 61
Qy 61 AHCSGSVWVRLGRHSLSDLTQWTEQIRHSGFSVT- ---HPGY---LGASTSHEHDLRLR 113
Db 62 AHCKRPVWVRLGRHSLSDLTQWTEQIRHSGFSVT- ---FRVTDPPHFGFNKDLNAN-DHDDIMLIR 116
Qy 114 LRLPVRVTSVQPLPNDCATAGTCRVSGWGITNHPNPPDQLQCLNLSIVSHATCH 173
Db 117 LPRQARLSPAVQPLNLSQTCVSPGWQCLISGWGAVSPKALFPVTLQCANISILENKLCH 176
Qy 174 GVYPRITSNMVCAG-GVPGQDACGDSGGPLVCGVLOGLVSMGSGVCGQDGIPIGVYT 232
Db 177 WAYFGHISDSMLCAGLWEGGRGSCGDSGGPLVCGVLOGLVSMGSGVCGQDGIPIGVYT 235
Qy 233 YICKYVDWIRMN 247
Db 236 SVCHYLDWIQEIMEN 250

RESULT 10
KLK9 HUMAN
ID_KLK9 HUMAN STANDARD; PRT; 277 AA.
AC Q9UKR3; Q9Y433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
DB (KLK-L4).
GN KLK13 OR KLK14.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```



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FT SIGNAL 1 15 BY SIMILARITY.
FT PROPEP 16 25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 26 248 TRYPSIN I-P38.
FT ACT SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT METAL 77 77 CALCIUM (BY SIMILARITY).
FT METAL 79 79 CALCIUM (VIA CARBONYL OXYGEN)
      (BY SIMILARITY).
FT METAL 87 87 CALCIUM (BY SIMILARITY).
FT ACT SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32 162 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 134 235 BY SIMILARITY.
FT DISULFID 141 208 BY SIMILARITY.
FT DISULFID 173 187 BY SIMILARITY.
FT DISULFID 198 222 BY SIMILARITY.
FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 248 AA; 26087 MW; 78879DD6PE15FOCE CRC64;

Query Match 41.2%; Score 566; DB 1; Length 248;
Best Local Similarity 45.8%; Pred. No. 2e-39;
Matches 116; Conservative 39; Mismatches 86; Indels 12; Gaps 7;

Qy 3 LSIFLLLCVLG-----LSQAATPKIFNTECGRNSQPMQVGLPEGTSLRCGGVLIDHRW 56
Db 1 MKFLVLVAFGLGVAVFPISEDDDDKIVGGYSCARSAAPYQVSLNSGYHP-CGGSLSISSQW 59
Qy 57 VLTAAHCGSGRYVRLGHEHSLSDMTQETRHSGFVTHPGYLGASTSHEHDLRLRL 116
Db 60 VLSAAHCYKSSIQVKGLEYNLAAQDGEQTISSSKVIRHSGY-NANTLN-NDIMLIKLSK 117
Qy 117 PVRVTSVQPLPLPNDCATAGTECHVSGMGITNHPNPPFDLLQCLNLSIVSHATCHGVY 176
Db 118 AATLNSYVNTVPLPTSCVTAGTTCCLISGMGNTLSSGSLYPDVLCNAPVLSSSQCSAY 177
Qy 177 PGRITSNMVCAGGV-PQODACQDSGGPLVCGVGLGWSGVPQCGQDGPVYTYIC 235
Db 178 PGRITSNMVICGYLNGKQSGDGGPVCNGLQGVSMG-IG-CAQKGYPGVYTKVC 235
Qy 236 KYVDWIRMIRNN 248
Db 236 NYVSWIKTWMSSN 248

RESULT 12
TRY1 CHICK STANDARD; PRT; 248 AA.
AC Q30627;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Pancreas;
RA MEDLINE=95251611; PubMed=7733885;
RT Wang K., Gan L., Lee I., Hood L.E.;
RT "Isolation and characterization of the chicken trypsinogen gene
family."
RL Biochem. J. 307:471-479(1995).
CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Xaa, Lys-Xaa.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: High levels are seen in the pancreas while
lower levels are found in the liver, spleen and thymus.
CC -I- SIMILARITY: Belongs to peptidase family S1.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U15155; AAA79912.1; -.
CC PIR; S55067; S55067.
CC HSP; P00763; 1DPO.
CC MEROPS; S01.151; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR001254; Peptidase-S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydroxylase; Serine protease; Digestion; Pancreas; Zymogen;
KW Calcium-binding; Signal; Multigene family.
FT SIGNAL 1 15 BY SIMILARITY.
FT PROPEP 16 25 ACTIVATION PEPTIDE (BY SIMILARITY).
FT CHAIN 26 248 TRYPSIN I-P1.
FT ACT SITE 65 65 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT METAL 77 77 CALCIUM (BY SIMILARITY).
FT METAL 79 79 CALCIUM (VIA CARBONYL OXYGEN)
      (BY SIMILARITY).
FT METAL 87 87 CALCIUM (BY SIMILARITY).
FT ACT SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32 162 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 134 235 BY SIMILARITY.
FT DISULFID 141 208 BY SIMILARITY.
FT DISULFID 173 187 BY SIMILARITY.
FT DISULFID 198 222 BY SIMILARITY.
FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SQ SEQUENCE 248 AA; 26069 MW; C4CF589912B23D98 CRC64;

Query Match 41.1%; Score 565; DB 1; Length 248;
Best Local Similarity 45.5%; Pred. No. 2.4e-39;
Matches 115; Conservative 41; Mismatches 85; Indels 12; Gaps 7;

Qy 3 LSIFLLLCVLG-----LSQAATPKIFNTECGRNSQPMQVGLPEGTSLRCGGVLIDHRW 56
Db 1 MKFLVLVAFGLGVAVFPISEDDDDKIVGGYSCARSAAPYQVSLNSGYHP-CGGSLSISSQW 59
Qy 57 VLTAAHCGSGRYVRLGHEHSLSDMTQETRHSGFVTHPGYLGASTSHEHDLRLRL 116
Db 60 VLSAAHCYKSSIQVKGLEYNLAAQDGEQTISSSKVIRHSGY-NANTLN-NDIMLIKLSK 117
Qy 117 PVRVTSVQPLPLPNDCATAGTECHVSGMGITNHPNPPFDLLQCLNLSIVSHATCHGVY 176
Db 118 AATLNSYVNTVPLPTSCVTAGTTCCLISGMGNTLSSGSLYPDVLCNAPVLSSSQCSAY 177
Qy 177 PGRITSNMVCAGGV-PQODACQDSGGPLVCGVGLGWSGVPQCGQDGPVYTYIC 235
Db 178 PGRITSNMVICGYLNGKQSGDGGPVCNGLQGVSMG-IG-CAQKGYPGVYTKVC 235
Qy 236 KYVDWIRMIRNN 248
Db 236 NYVSWIKTWMSSN 248

RESULT 13
KLK5 HUMAN STANDARD; PRT; 293 AA.
ID KLK5 HUMAN
AC Q9Y337; Q9HGB8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)

```


DE Kallikrein 5 precursor (EC 3.4.21.-) (Stratum corneum tryptic enzyme)
GN KLIK5 OR SCTE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stratum corneum;
RA MEDLINE=99445563; PubMed=10514489;
RX Bratteland M., Egelrud T.;
RT "Purification, molecular cloning, and expression of a human stratum
corneum trypsin-like serine protease with possible function in
desquamation.";
RL J. Biol. Chem. 274:30033-30040(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20118156; PubMed=10652563;
RA Yousef G.M., Luo L.-Y., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome
19q13.3-q13.4.";
RL Anticancer Res. 19:2843-2852(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20510030; PubMed=11054574;
RA Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
RT Moss P., Paepel B., Wang K.;
RA "Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
RL Gene 257:119-130(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May be involved in desquamation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed in skin, breast, brain and testis.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AF168768; AAF03101.1; -;
DR EMBL; AF135028; RAD26429.1; -;
DR EMBL; AP243527; AAG33358.1; -;
DR EMBL; BC008036; AAH08036.1; -;
HSSP; P00763; IDPO.

DR MEROPS; S01.017; -;
DR Genew; HGNC:6366; KLIK5.
DR MIN; 605643; -;
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004252; P:serine-type endopeptidase activity; NAS.
DR GO; GO:0008544; P:epidermal differentiation; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 293 KALLIKREIN 5.
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 153 153 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 245 245 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 73 206 BY SIMILARITY.
FT DISULFID 93 109 BY SIMILARITY.
FT DISULFID 178 279 BY SIMILARITY.
FT DISULFID 185 251 BY SIMILARITY.
FT DISULFID 217 231 BY SIMILARITY.
FT DISULFID 241 266 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 25 56 MISSING (IN REF. 3).
SQ SEQUENCE 293 AA; 32020 MM; D92C92F5609E5946 CRC64;

Query Match 41.1%; Score 564.5; DB 1; Length 293;
Best Local Similarity 45.3%; Pred. No. 3.2e-39;
Matches 107; Conservative 41; Mismatches 83; Indels 5; Gaps 4;

QY 15 SQAATPKIFNTEGGRNSQPMQVG-LFEGTSLRCGGVLIDHRWLVTAHCSGRYVRLG 73
DB 60 SDDSSRIINGSDCDMTQWQALLRPNLQYGVLPQWLLTAHCRKKVPRVLG 119

QY 74 EHSLSQLDWTQIRHSGF-SVTHPGYLGASTSHEDLRLRLPVRVTSVQPLPLND 132
DB 120 HYSLSVPYBSQQMFGQVKSIPHPGY--SHPGHSNDLMLIKLNRIRPTKDVPRINVS 177

QY 133 CATAGTECHVSGWGITNHPRPFPDULLQCLNLSVSHATCHGVYGRITSNVACAGVPG 192
DB 178 CPSAGTKCLVSGWGTTSKSPQVHPFKVQLCLNLSVLSQKRCEDAYPRQIDDTMFCAGD 237

QY 193 QDACQGSQGGPLVCGVLQGLVSGSVGPGCGQDGIPIGVYVYICKYVDMIRMIRN 248
DB 238 RDSQCQSGSGPVCNGLSGLVSWGDY-PCARNRPNRGVYTNLCKETKTIQETIOAN 292

RESULT 14
KLIK5 HUMAN STANDARD; PRT; 276 AA.
AC O43240; O99920; O9GZM9;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Kallikrein 10 precursor (EC 3.4.21.-) (Protease serine-like 1) (Normal
epithelial cell-specific 1).
GS KLIK5 OR PRRS1 OR NES1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epithelium;

DT 01-NOV-1997 (Rel. 35, Last sequence update)
DB 10-OCT-2003 (Rel. 42, Last annotation update)
OS Trypsin precursor (EC 3.4.21.4)
OC Xenopus laevis (African clawed frog)
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang K., Lytle L., Can L., Hood L.R.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBSJ databases.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U72330; AAB17274.1; -.
DR HSP; P00763; IDPO.
DR MEROPS; S01.258; -.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Digestion; Zymogen; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 15
FT PROPEP 16 21
FT CHAIN 22 244
FT ACT_SITE 61 61
FT METAL 73 73
FT METAL 75 75
FT METAL 83 83
FT ACT_SITE 105 105
FT DISULFID 28 158
FT DISULFID 46 62
FT DISULFID 130 231
FT DISULFID 137 204
FT DISULFID 169 183
FT DISULFID 194 218
FT SITE 192 192
FT SITE 192 192
SQ SEQUENCE 244 AA; 26079 MW; C63P29C93300B323 CRC64;
Query Match 41.0%; Score 563; DB 1; Length 244;
Best Local Similarity 45.0%; Pred. No. 3.5e-39;
Matches 112; Conservative 46; Mismatches 83; Indels 8; Gaps 5;
QY 3 LSIFLLLCVLGLSQA--ATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWVLTA 60
DB 1 MKFLVILVLLGAVAFEDDDKIVGGFTCAKNAPVQVSLNAGVHP-CGSSLINSQWVSA 59
QY 61 AHCSSGRYWRVLRGSHLSOLDWTEQIRHSGFVTHPGYLGASTSHSHDLRLRLPLRVV 120
DB 60 AHCYKSRIVRLGERHIALNEGTEQIDSKVKKHPNY--NSRNLNDIMLIKLSSTARL 117
QY 121 TSSVQPLPLPNCATAGTCHVSGGITHNPRNPDPDLLOCLNLSVSHATCHGVYVGR 180
DB 118 SANIQSVPLPSACASAGTNCCLISGWNLTUSGTNTPDLLQCLNAPILTDSCNSYPG 177

QY 181 TSNMVCAGGVP-GQDACQGDSSGSPVCGGVLOGLVSMGSGVPCGGDGIPIGVVYI CKYVD 239
DB 178 TKMFCAGFLAGKXKSCQGDSSGSPVCGGVLOGLVSMGSGVPCGGDGIPIGVVYI CKYVD 235
QY 240 WIRMIMRN 248
DB 236 WQSTISSN 244

Search completed: June 16, 2004, 15:05:20
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:02:10 ; Search time 45 Seconds
(without alignments)
1738.856 Million cell updates/sec

Title: US-10-006-116A-194
Perfect score: 1374
Sequence: 1 MGLSIFLLCVGLSLQAATP.....GVVYICKYVDWIRMIRNN 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	952.5	69.3	234	11 Q9CV76	Q9cv76 mus musculus
2	627.5	45.7	260	4 Q8IM69	Q8im69 homo sapien
3	608	44.3	254	11 Q8CGR4	Q8cgr4 mus musculus
4	601	43.7	275	4 Q8IXD7	Q8ixd7 homo sapien
5	597.5	43.5	249	11 Q9QYN4	Q9qyn4 mus musculus
6	597.5	43.5	276	11 Q9QYN3	Q9qyn3 m hippostas
7	595	43.3	255	4 Q96RQ0	Q96rq0 homo sapien
8	598.5	42.8	293	11 Q9D140	Q9d140 mus musculus
9	588	42.8	276	11 Q8CGR6	Q8cgr6 mus musculus
10	586	42.6	250	11 Q8CGR5	Q8cgr5 mus musculus
11	578	42.1	242	11 Q8QV54	Q8qv54 mus musculus
12	563	41.0	248	13 Q7SZT1	Q7szt1 xenopus lae
13	555	40.4	243	13 Q7SZ06	Q7sz06 xenopus lae
14	553.5	40.3	246	11 Q88301	Q88301 mus musculus
15	553.5	40.3	253	11 Q91Y82	Q91y82 mus musculus
16	550.5	40.1	247	11 Q9D7Y7	Q9d7y7 mus musculus

17	549.5	40.0	247	11 Q9CPN9	Q9cpn9 mus musculus
18	546.5	39.8	251	11 Q54854	Q54854 rattus norv
19	544	39.6	253	4 Q8NSN9	Q8nsn9 homo sapien
20	541.5	39.4	247	11 Q9CPN7	Q9cpn7 mus musculus
21	538.5	39.2	249	11 Q91VE3	Q91ve3 mus musculus
22	536	39.0	246	11 Q9ROT7	Q9rot7 mus musculus
23	536	39.0	246	11 Q7TT42	Q7tt42 mus musculus
24	533	38.8	246	11 Q9ZIR9	Q9zir9 mus musculus
25	532	38.7	246	11 Q9QUK9	Q9quk9 mus musculus
26	525	38.2	240	13 Q98TH0	Q98th0 engraulis j
27	522	38.0	244	13 Q8QGW3	Q8qgw3 anguilla ja
28	514.5	37.4	242	13 Q7TIR8	Q7tir8 pangasius h
29	514	37.4	239	11 Q63275	Q63275 rattus norv
30	513.5	37.4	243	13 Q8AV83	Q8av83 brachydanio
31	513.5	37.4	261	6 Q9NIQ1	Q9niq1 saguinus oe
32	513.5	37.4	278	11 Q99M20	Q99m20 mus musculus
33	511.5	37.2	261	6 Q29474	Q29474 canis famil
34	510.5	37.2	238	13 Q9W7Q6	Q9w7q6 paralicthy
35	509.5	37.1	222	13 Q8AV11	Q8av11 oncorhynch
36	509.5	37.1	235	11 Q63274	Q63274 rattus norv
37	508	37.0	242	13 Q9W7Q7	Q9w7q7 paralicthy
38	507	36.9	244	13 Q42159	Q42159 petromyzon
39	506	36.8	245	13 Q42160	Q42160 petromyzon
40	505	36.8	242	13 Q7SX90	Q7sxn0 brachydanio
41	505	36.8	249	13 Q92046	Q92046 disceotichu
42	504.5	36.7	269	4 Q8IU55	Q8iuss homo sapien
43	503	36.6	241	13 Q98TG9	Q98tg9 engraulis j
44	502	36.5	249	13 Q9W6K0	Q9w6k0 notothenia
45	501.5	36.5	237	13 Q91515	Q91515 fuigu rubrip

ALIGNMENTS

RESULT 1

Q9CV76	ID	Q9CV76	PRELIMINARY;	PRT;	234 AA.
AC	Q9CV76;				
DT	01-JUN-2001	(TRMBLrel. 17, Created)			
DT	01-JUN-2001	(TRMBLrel. 17, Last sequence update)			
DT	01-OCT-2003	(TRMBLrel. 25, Last annotation update)			
DE	2310008B01RIK	protein (Fragment).			
GN	2310008B01RIK.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CS7BL/6J; TISSUE=Tongue;				
RX	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikolaic I., Pesole G., Quackenbush J.,				
RA	Sakai K., Stabili P., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Schriml L.M., Stauber P., Suzuki R., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,				
RA	Hayashizaki Y.;				
RL	"Functional annotation of a full-length mouse cDNA collection."				
RL	Nature 409:685-690(2001).				
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.				
DR	EMBL; AK009217; BAB26143.1; -.				


```
QY 63 CSRSRYWVRLGHSLSQLDWTEQIRHSFSGSVTHPGYLGASTSHSHDLRLRLPLRVVTS 122
DB 61 CQTRFMVRVLGEHLNRKFDGPEQLRSVRRIIPFGY--EARTHEDIMLLRLFKPARLTA 118
QY 123 SVQPLPLPNDCATAGTECHVSGHGIYTHPRNP-----FPDLLOCLNLSIVSHAT 171
DB 119 YRVPALPRCLPGLGDCVSVGGLLS-DNPNPGATGSKSHVRLPDTLHCANISIIISRAS 177
QY 172 CHGVYPERITSNMVCV---GGVPGQACQDSCGPLVCGVLQGLVSGVSGVPGCGDGIP 228
DB 178 CNKDYFGRVLPTWVCAGVEGG--GTDSCEGDSGPLVCGGALAGIYVSGVDV-PCDTTTPK 234
QY 229 GVTYICKYVDWI 241
DB 235 GVTYKVCYLEWI 247

RESULT 4
Q8IXD7
ID Q8IXD7 PRELIMINARY; PRT; 275 AA.
AC Q8IXD7
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Variant form hippostasin/KLX11.
GN KLX11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Nakamura T., Mitsui S., Miki T., Yamaguchi N.;
RT "Molecular cloning and expression of a variant form of
RL hippostasin/KLX11 in prostate.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB078780; BAC54105.1;
DR GO; GO:0004263; F-tyrosinase activity; IEA.
DR GO; GO:0004295; F-tyrosinase activity; IEA.
DR GO; GO:0006508; Proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;

Query Match 43.7%; Score 601; DB 4; Length 275;
Best Local Similarity 44.2%; Pred. No. 5.5e-50;
Matches 121; Conservative 35; Mismatches 88; Indels 30; Gaps 5;

QY 3 LSIFLLLCVLGLSQAATPKIFNGTECGRNQSPQVGLFEGTSLRCGVLIDHRWLTAH 62
DB 4 LQILLALATGLVGGET-RIIKFECXPHSQPQWQALFEKTRLLCGATLAPKLLTAH 62
QY 63 CSG-----SRYVRLGHSLSQLDWTEQIRHSFSGSVTHPG 97
DB 63 CLXPSWLTSPHTVSPDLSNVCLSHLRYIVHLGQHNLQKEGCGTRTATESPPHPG 122
QY 98 YLGA--STSHEDLRLRLPLRVVTSVQPLPNDCATAGTECHVSGHGIYTHPRNP 155
DB 123 FNNSLPKDHRNDIMLVKMAAPSVITWAVRPLTLSSRCVTAAGTSLISGWSGSTSSPOLRL 182
QY 156 PDLLOCLNLSIVSHATCHGVYKRTITSNMVCAG-GVPGQACQDSCGPLVCGVLQGLV 214
DB 183 PHLRCANITIIIEHQKCNAYPGNITDNTWCASVQEGGKDCQDSCGPLVCGSLQGLII 242
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QY 215 SMGSVQPCQDGIPIGVYTYICKYVDWIRMIMRNN 248
DB 243 SMQD-DPCATTRKPGVYTYICKYVDWIQETMGN 275

RESULT 5
Q9QYN4
ID Q9QYN4 PRELIMINARY; PRT; 249 AA.
AC Q9QYN4
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hippostasin.
GN PRSS20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Yamaguchi N., Mitsui S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning of a novel brain serine protease, Hippostasin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016226; BAA88825.1;
DR HSSP; P00763; IDP0.
DR MEROPS; S01.257; -.
DR GO; GO:0005576; C-extracellular; IDA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 249 AA; 27604 MW; F9FP9CB457D727D5 CRC64;

Query Match 43.5%; Score 597.5; DB 11; Length 249;
Best Local Similarity 47.0%; Pred. No. 1.1e-49;
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;

QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNQSPQVGLFEGTSLRCGVLIDHRWLTA 60
DB 1 MILRLIALALVTGHVGGET-RIIKGYECRPHSQPQWQALFQKTRLLCGATLIAPKLLTA 59
QY 61 AHCSGRYVWVRLGHSLSQLDWTEQIRHSFSGSVTHPGYLG--STSHEDLRLRLPLV 118
DB 60 AHCRKPHYVTLLEHNLKTDGCGEQRMMATESPPHPDNNLSLPNDHRNDIMLVKMSPV 119
QY 119 RVTSSVQPLPLPNDCATAGTECHVSGHGIYTHPRNPFPDLLOCLNLSIVSHATCHGVY 178
DB 120 FFRVAQPLTSLPHCVAACTSLISGWTSSPOLRLPHSLRCANVSIIHKECEKAYPG 179
QY 179 RITSNMVCAG-GVPGQACQDSCGPLVCGVLQGLVSGVSGVPGCGDGIPGVYTYICKY 237
DB 180 NITDVTMLCASVRKEGKDCQDSCGPLVCGSLQGLIISWQD-DPCAVTRKPGVYTYICKY 238
QY 238 VDWIRMIMRNN 248
DB 239 FNNIHEVMRNN 249

RESULT 6
Q9QYN3
ID Q9QYN3 PRELIMINARY; PRT; 276 AA.
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AC Q9QYN3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hipocastin prostate type (Adult male tongue cDNA, RIKEN full-length
DE enriched library, clone:2310015108 product:protease, serine, 20, full
DE insert sequence) (Adult male tongue cDNA, RIKEN full-length enriched
DE library, clone:2310040P07 product:protease, serine, 20, full insert
DE sequence).
GN PRS20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Yanaguchi N., Mitsu S.
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Yanaguchi N., Mitsu S.
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu M., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Katsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Onno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA The PANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA MEDLINE=99279253; PubMed=10349636;
RX Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [8]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Kagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB016227; BAA36955.1; -;
DR EMBL; AK009360; BAB26241.2; -;
DR EMBL; AK009720; BAB26461.2; -;
DR HS9P; P00763; IDPO.
DR MEROPS; S01.257; -;
DR MG; MG1:1929977; Press20.
DR GO; GO:0005576; C:extracellular; IDA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin_1
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00240; TRYPsin DOM; 1.
DR PROSITE; PS00134; TRYPsin HIS; 1.
DR PROSITE; PS00135; TRYPsin SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 276 AA; 30753 MW; 90BDC03A8AB178D6 CRC64;
Query Match 43.5%; Score 597.5; DB 11; Length 276;
Best Local Similarity 47.0%; Pred. No. 1.2e-49;
Matches 118; Conservative 33; Mismatches 95; Indels 5; Gaps 4;
QY 1 MGLSIFLLCVLGLSQAATPKIPNGTEGRNSQPMQVGLFEGTSLRCGVLIDHRWVLT 60
DB 28 MLRLIALALVTGHVGGST-RIIKGYECPHSQPMQVALFQKTRLLCGATLAPKWL 86
QY 61 AHCSGSYVVRGLGHSLSQLOWTEQIRHSGFVTHPGVLGA--STSHEDHLRLRLP 118
DB 87 AHCRKPHYVILLGHNLEKTCCEQRNATSFPPDFPNSLPNKDNDIMLVKSSPV 146
QY 119 RVTSSVQPLPLPNDCATAGTECHVSGMGITNHRNPPFPDLQCLNLSIVSHATCGVY 178
DB 147 PFTRAVQPLTLSPHCVAAGTSLISGWTSSPQLRLPHSLRCANVSIIHKKECKAY 206
QY 179 RITSNNVCAG-GVPGQDACQDSGGLVCGGVQLGVLSVSGVPGCGDGIKGVYTVICKY 237
DB 207 NITDTMLCASVRKEGKDSQDSGGLVCGVLSQGIISWGQ-DPCAVTRKPGVYTVICKY 265
QY 238 VDWTRIMRN 248
DB 266 FNVHIVMRN 276
RESULT 7
Q96RQ0 PRELIMINARY; PRT; 255 AA.
AC Q96RQ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Prostinogen.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21226193; PubMed=11327827;

RA Takayama T.K., Carter C.A., Deng T.;
RT "Activation of prostate-specific antigen precursor (pro-PSA) by
RT prostatin, a novel human prostatic serine protease identified by
RT degenerate PCR.";
RL Biochemistry 40:1679-1687(2001).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF303046; AAK62813.1; -;
DR HSSP; P00761; IANI.
DR MEROPS; S01.081; -;
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 255 AA; 27986 MW; 00DSB79E14B9468F CRC64;
Query Match 43.3%; Score 595; DB 4; Length 255;
Best Local Similarity 46.3%; Pred. No. 1.9e-49;
Matches 119; Conservative 32; Mismatches 87; Indels 18; Gaps 6;
QY 8 LLVGLSQAAT----PKIFNGTECGRNSQFQWGLPEGTSLRGGVLIDHRVWLTAAHC 63
DB 3 LLTSLFLASTAQDGDGLLEGDECAHPSQWQVALYERFNGASLSPHWVLSAHC 62
QY 64 SGRYVVRLEHSLQDTEQIRHSGFSVTHPGYLGASTSHEDLRLRLPVRVTS 123
DB 63 QSRFMRVRLGEHLRKEDEQEQLRTSRVTPHRY--EARSHERDMLGLVQPARLNQ 120
QY 124 VQPLPLPNDCAATAGTECHVSGWITWY-----PRN--PFDLQCLNLSIVSHATCH 173
DB 121 VRPAVLPTRCPPHGEACVWVGWLSHNEFGTAGSPRSQVSLPDTLHCANIGIISDSCD 180
QY 174 GVTPGRITSNMVCAGV-PQDACAQDSGGPLVCGVLQGLVSWGSGVPCQGDGIPGVYT 232
DB 181 KSPFGLTNMVCAGREGRAESCEGDSGGLVCGVLQGLVSWGSDV-PCDNTTKGVYT 239
QY 233 YICKYVDWIRIMRNN 248
DB 240 KVCHYLEWIRETKRN 255
RESULT 8
Q9D140
ID Q9D140 PRELIMINARY; PRT; 293 AA.
AC Q9D140;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110030019Rik protein.
GN 1110030019RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli P., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AK003996; BAB23113.1; -;
DR HSSP; P00763; IDPO.
DR MEROPS; S01.017; -;
DR MEROPS; S01.418; -;
DR MGD; MGI:1915918; 1110030019Rik.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolyase; Protease; Serine protease.
SQ SEQUENCE 293 AA; 31908 MW; ED1F45D8226FE911 CRC64;
Query Match 42.8%; Score 588.5; DB 11; Length 293;
Best Local Similarity 47.2%; Pred. No. 9.5e-49;
Matches 110; Conservative 41; Mismatches 77; Indels 5; Gaps 4;
QY 18 ATPKFNTECGRNSQFQWGLPEG-TSLRCGGVLIDHRVWLTAAHCSGRYVRLGHS 76
DB 64 SSSRIVNGSDCKDAQWQCALGPNKLYCGAVLISQWMLTAAHCKPVRIRLGHSS 123
QY 77 LSQDTEQIRHSGP-SVTHPGYLGASTSHEDLRLRLPVRVTSVQPLPNDCA 135
DB 124 MSPVYESGQMFQGIKSIHPGY--SHPGHNDMLIKNRKIRDSHVKEVETACD 181
QY 136 AGTECHVSGWITNHPNPPDLQCLNLSIVSHATCHGVTPGRITSNMVCAGVPGDA 195
DB 182 EGRCHVSGWITNHPNPPDLQCLNLSIVSHATCHGVTPGRITSNMVCAGVPGDA 241
QY 196 CQGDGGLVCGVLQGLVSWGSGVPCQGDGIPGVYTYICKYVDWIRIMRNN 248
DB 242 CQGDGGLVCGVLQGLVSWGDF-PCAQRNRRFGVYTNLCEPVKRWIKDTMNSN 293
RESULT 9
Q8CGR6
ID Q8CGR6 PRELIMINARY; PRT; 276 AA.
AC Q8CGR6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glandular kallikrein KLK13.
GN KLK13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundwall A.,


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RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus."
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY152432; AAN78420.1; -.
DR MGD; MGI:95292; K1K13.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDCA CRC64;

Query Match 42.8%; Score 588; DB 11; Length 276;
Best Local Similarity 46.3%; Pred. No. 9.9e-49;
Matches 120; Conservative 38; Mismatches 81; Indels 20; Gaps 7;

QY 8 LLCV-LGLSQAT---PKIFNGTE-----CGNSOPQVGLFEGTSLRCGGVLI 52
DB 8 IACUTALALSEGISRDYPKILNNTGNTSGFLPGGYTCLPHSQPQAAILIRGLLCGGVLI 67

QY 53 DHRWLTAAHCSGRYVWLRLGHSLSQLDWTQIRHSQSVTHPGYLCGAST--SHEHDLR 110
DB 68 HPKWLTLAAHCKDGYTHLGHGLRVENGQAMQEVVRSIPHPYQVTPHNLNHDHIM 127

QY 111 LRLRLPVRVTSVQPLPL-PNDCAATAGTECHVSGWGIITHNRPNPPDLLQCLNLSIVSH 169
DB 128 LLELKSPVQLSSHVRTLKLSADDCPLPTGTCRCVSGWGTTSQVNVYPTKLQCANIELRSD 187

QY 170 ATCHGVYFGRITSNMVCAGVGP-GQDACQSDSGPLVCGVLCGLVSGVSPGCCQDGIP 228
DB 188 EECRVYFGKITANMLCAGTKEGGKDSCEGDSGLNCKGLYIISWGDV-PCGQPNRP 246

QY 229 GYTVYICKYVDWIRMN 247
DB 247 GYTVYICKYVDWIREIIN 265

RESULT 10
Q8CGR5 PRELIMINARY; PRT; 250 AA.
AC Q8CGR5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glandular kallikrein K1K14.
GN K1K14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22325484; PubMed=12437987;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RT musculus."
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY152433; AAN78421.1; -.

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DR MGD; MGI:2447564; K1K14.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 250 AA; 27016 MW; F62FBBF2290FBB8 CRC64;

Query Match 42.6%; Score 586; DB 11; Length 250;
Best Local Similarity 47.2%; Pred. No. 1.4e-48;
Matches 120; Conservative 40; Mismatches 80; Indels 14; Gaps 7;

QY 5 IFLLLCVL-----GLSQA-ATPKIFNGTECGRNSQVQVGLFEGTSLR--CGVLIDHRW 56
DB 1 MFLLLIILQALAVAIQAQSGDHKIIIGYRCVRSQVQVVALQAGPGHREFLCGVLISDQW 60

QY 57 VLTAAHCSGRYVWLRLGHSLSQLDWTQIRHSQSVTHPGYLCGASTSHEHDLRLRLRL 116
DB 61 VITRAHCAARPIHLVALGKHNRIRWEATQVVRVQVPHQY--QPAAHNDMLLKLQK 118

QY 117 PVRVTSVQPLPLPNDCAATAGTECHVSGWGIITHNRPNPPDLLQCLNLSIVSHATCHGVY 176
DB 119 KYRLGRAVKTISVASSCASPGTPCVRVSGWGTIASIARYPTALQCVNVNIMEQACHRAY 178

QY 177 PGRITSNMVCAGVGP--QGDACQSDSGPLVCGVLCGLVSGVSPGCCQDGIPGVYTYI 234
DB 179 PGLITSGMVCA-GVPEGGKDSQCGSGPLVCGGQLQGLVSWG-MERCAMPYGPVGVYANL 236

QY 235 CKYVDWIRMN 248
DB 237 CNYHSWIQRTMQSN 250

RESULT 11
Q8QVS4 PRELIMINARY; PRT; 242 AA.
AC Q8QVS4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to kallikrein 14 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NMRI; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC044756; AAH44756.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 242 AA; 26059 MW; A3F8A624DB481D36 CRC64;

```



```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054194; AAH54194.1; -.
KW Hypothetical protein.
SQ SEQUENCE 243 AA; 25476 MW; C5B82B458B209F31 CRC64;

Query Match 40.4%; Score 555; DB 13; Length 243;
Best Local Similarity 45.7%; Pred. No. 1.3e-45;
Matches 113; Conservative 42; Mismatches 82; Indels 10; Gaps 6;

Qy 6 FLLCVLGLSQAAT---PKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRVWLTAAH 62
Db 3 FLLCVL-LGAAAFDDDDKIIGATCAKSSVPYIVLSNGYHF-CGSLITNQWVSAAH 60

Qy 63 CSGSRVYVRLGHSLSQLDWTEQIRHSGFSPVTHPGYLGASTSHEHDLRLRLPVRVTS 122
Db 61 CYKASIQVRLGHNLAUSEGTEQFISSKVIHSGY--NSYTLNDIMLIKLSFASLNA 118

Qy 123 SVQPLPLPNDCATAGTECHVSGMGITNHPRPFPDLQLCLNLSIVSHATCHGVYVPGRIITS 182
Db 119 AVNTVPLPSGCSAAGTSLISGWNLTLSNGSNYPDLQLCLNAPILTNAQCNAYSYPGEITA 178

Qy 183 NMVCAGGV-PGDACQDGSGLVCGGVQLGVLGWSVGPCCQDGIPOGVYTYICKYVDWI 241
Db 179 NMICVGFEGKDSQCGDGGPVVCGNLQGVWSNGY--GCAMRNPYGVYTKVNTYNAWI 236

Qy 242 RMIMRN 248
Db 237 QNTAAN 243

RESULT 14
O88301 PRELIMINARY; PRT; 246 AA.
ID O88301;
AC O88301;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine protease (BSP).
GN PRS18 OR MBSP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Matsui H., Takahashi T.;
RT "Mouse serine protease preferentially expressed in brain.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Skin;
RA Meier N., Dear T.N., Boehm T.;
RT "A novel serine protease expressed in the hair follicle.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Matsui H., Takahashi T.;
RT "The sequences of mouse serine protease gene expressed in brain.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB015206; BAA28895.1; -.
DR EMBL; Y18723; CAA77269.1; -.
DR EMBL; AB032402; BAA84544.1; -.
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prss18.

GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TRYPSIN_SPC; 1.
PROSITE; PS02040; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; protease; Serine protease.
SQ SEQUENCE 246 AA; 27496 MW; E20C0808087139B63 CRC64;

Query Match 40.3%; Score 553.5; DB 11; Length 246;
Best Local Similarity 43.5%; Pred. No. 1.9e-45;
Matches 107; Conservative 46; Mismatches 82; Indels 11; Gaps 6;

Qy 7 LLLCVLGLSQA---TPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRVWLTAAH 62
Db 4 LALCLV-LAKSAWSEBQKVVHGGPCLKDSHPFOALYTSGLHLCGGVLIDPQWVLTAAH 62

Qy 63 CSGSRVYVRLGHSLSQLDWTEQIRHSGFSPVTHPGYLGASTSHEHDLRLRLPVRVTS 122
Db 63 CKKPNLVILGKHNLRQTFETFOISVDRTIVHPRY--NPETHNDIMMVHLKNPVKFSK 120

Qy 123 SVQPLPLPNDCATAGTECHVSGMGITNHPRPFPDLQLCLNLSIVSHATCHGVYVPGRIITS 182
Db 121 KIQPLPLKNDCEENPNCQILGNG--KNENGDFDTIQCADVHLVPRQCERAYPGKITQ 178

Qy 183 NMVCAGGV-PGDACQDGSGLVCGGVQLGVLGWSVGPCCQDGIPOGVYTYICKYVDWI 241
Db 179 SVMCAGDKCKGDSQCGDGGPVVCGNLQGVWSNGDM-PCGSKEKPGVYTDVCTHIRWI 237

Qy 242 RMIMRN 247
Db 238 QNILRN 243

RESULT 15
O91Y82 PRELIMINARY; PRT; 253 AA.
ID O91Y82;
AC O91Y82;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neurosin (Protease, serine, 18).
GN PRS18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning and characterization of mouse brain specific serine
protease, Neurosin.";
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB008928; BAB5605.1; -.
DR EMBL; BC031119; AAH31119.1; -.
DR HSSP; P00761; IANI.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prss18.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:06:56 ; Search time 60 Seconds
(without alignments)
1167.863 Million cell updates/sec

Title: US-10-006-116a-194

Perfect score: 248
Sequence: 1 MGUSIFLLLCVLGSLQAATP.....GVVTYICKYVDWIRMNRNN 248

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	100.0	248	3	AAB21304 Human KLK
2	248	100.0	248	3	AAB24428 Human PRO
3	248	100.0	248	3	AAB24032 Human PRO
4	248	100.0	248	3	AAY99393 Human PRO
5	248	100.0	248	4	AAM23994 Human EST
6	248	100.0	248	4	AAB66142 Protein o
7	248	100.0	248	6	ABO33635 Novel hum
8	248	100.0	248	7	ABO44488 Human sec
9	248	100.0	248	7	ABO33512 Novel hum
10	248	100.0	248	7	ADC18063 Human PRO
11	248	100.0	248	7	ADD70709 Human sec
12	248	100.0	248	7	ADD39786 Human sec
13	248	100.0	248	7	ADD70232 Human sec
14	248	100.0	248	7	ADD38353 Human sec
15	248	100.0	248	7	ADD39309 Human sec
16	248	100.0	248	7	ADD38832 Human sec
17	248	100.0	248	7	ADD40263 Human sec
18	248	100.0	248	7	ADE50484 Human sec
19	248	100.0	248	7	ADE20096 Human sec
20	248	100.0	248	7	ADE50007 Human sec
21	248	100.0	248	7	ADE21565 Human sec
22	235	94.8	254	3	AAB21303 Human KLK
23	235	94.8	254	5	ABG56676 Human nov
24	184	74.2	184	3	AAB21301 Human KLK
25	182	73.4	248	6	AAO29516 Human kal

26	93	37.5	162	2	AAY28642 Human sec
27	65	26.2	111	3	AAB21302 Human KLK
28	14	5.6	562	1	AAP70474 Sequence
29	13	5.2	30	3	AAB08953 Human sec
30	13	5.2	70	5	AAB76373 Human Mar
31	13	5.2	107	5	ABP09500 Human ORF
32	13	5.2	113	7	ADC31388 Human nov
33	13	5.2	117	1	AAP81986 Chain 2 o
34	13	5.2	187	3	AAY72094 Human ser
35	13	5.2	187	5	ABG30791 Human ser
36	13	5.2	187	5	ABE17922 Human gen
37	13	5.2	199	5	AU77550 Membrane-
38	13	5.2	212	2	AAY28590 Human fac
39	13	5.2	214	4	AAG79215 Consensus
40	13	5.2	217	6	ABO00751 Polypepti
41	13	5.2	226	5	AAB21442 Human try
42	13	5.2	226	6	ABG75786 Trypsin d
43	13	5.2	227	5	ABE14342 Human pro
44	13	5.2	227	6	ABG75785 Trypsin d
45	13	5.2	228	7	AAB39994 Human adi

ALIGNMENTS

RESULT 1
AAB21304
ID AAB21304 standard; protein; 248 AA.
XX
AC AAB21304;
XX
DT 02-FEB-2001 (first entry)
XX
DE Human KLK-L5 protein #4.
XX
KW Human; KLK-L1; KLK-L2; KLK-L3; KLK-L4; KLK-L5; KLK-L6;
KW kallikrein-like protein; serine protease; cytostatic; cancer;
KW prostrate cancer.
XX
OS Homo sapiens.
XX
PN W0200053776-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000MO-CA000258.
XX
PR 11-MAR-1999; 99US-0124260P.
PR 01-APR-1999; 99US-0127386P.
PR 21-JUL-1999; 99US-0144919P.
XX
PA (MOUN) MOUNT SINAI HOSPITAL.
XX
PI Yousef GM, Diamandis EP;
XX
WP1; 2000-587440/55.
DR N-PSDB; AAA95944.
XX
PT New kallikrein-like (KLK-L) proteins for diagnosing and treating KLK-L
XX protein mediated disorders, especially cancer.
XX
PS Claim 12; Page 172; 184pp; English.
XX
CC The present sequence is one of four alternatively spliced kallikrein-like
CC proteins encoded by the human KLK-L4 gene. Kallikreins and kallikrein-
CC like proteins are a subgroup of the serine protease enzyme family. They
CC catalyse the selective cleavage of specific polypeptide precursors to
CC release peptides with potent biological activity. Nucleic acids encoding
CC kallikrein-like proteins KLK-L1, KLK-L2, KLK-L3, KLK-L4, KLK-L5 and KLK-
CC L6 have been isolated. The proteins are useful in the treatment,
CC monitoring and diagnosis of cancers, especially prostate cancer. They
CC can also be used to identify a substance that can associate with or
CC mediate the biological activity of the proteins. Antibodies can be used

CC to treat conditions mediated by the kallikrein-like proteins

XX Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MGLSIFLLCVLGLSQAATPKIFNCTECGRNSQPMQVGLFECTSLRCGGVLIDHRWVLT 60
DB 1 MGLSIFLLCVLGLSQAATPKIFNCTECGRNSQPMQVGLFECTSLRCGGVLIDHRWVLT 60
OY 61 AHCSSRYVWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
DB 61 AHCSSRYVWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
OY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
OY 181 TSNMVCAGVPGQDACQDSGGPLVCGVLOGLVSGSVGPGQDGIPIGVYTYICKYVDW 240
DB 181 TSNMVCAGVPGQDACQDSGGPLVCGVLOGLVSGSVGPGQDGIPIGVYTYICKYVDW 240
OY 241 IRMIMRNN 248
DB 241 IRMIMRNN 248

RESULT 2

AAB24428
ID AAB24428 standard; protein; 248 AA.

XX AAB24428;

XX 07-NOV-2000 (first entry)

DE Human PRO1303 protein sequence SEQ ID NO:203.

XX Human; PRO; promotion; inhibition; angiogenesis; cardiovascularisation;
KW diagnosis; trauma; wound; cancer; atherosclerosis; cardiac hypertrophy;
KW angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic;
KW cytostatic; gene therapy; vaccine.

XX Homo sapiens.

XX WO200032221-A2.

XX 08-JUN-2000.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1998; 98WO-US025108.

XX 16-DEC-1998; 98US-0112850P.

XX 12-JAN-1999; 99US-0115554P.

XX 08-MAR-1999; 99WO-US005028.

XX 12-MAR-1999; 99US-0123957P.

XX 28-APR-1999; 99US-0131445P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Hillan KJ;
PI Goddard A, Godowski PJ, Gurney AL, Klein RD, Kuo SS, Paoni NF;
PI Smith V, Watanabe CK, Williams PM, Wood WI;

XX WPI; 2000-412154/35.

DR N-FSDB; AAB77671.

XX Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing
and treating diagnosing a cardiovascular, endothelial or angiogenic
disorders in mammals.

PS Claim 72; Fig 82; 315pp; English.

XX The present invention describes nucleic acids encoding PRO polypeptides
useful for preventing, diagnosing and treating diagnosing a
cardiovascular, endothelial or angiogenic disorder in mammals by
modulating cell proliferation, angiogenesis and cardiovascularisation,
and for identifying agonists and antagonists of these processes. The
nucleic acids and the proteins they encode may be used in the prevention,
treatment and diagnosis of diseases associated with inappropriate PRO
expression such as cardiovascular, endothelial or angiogenic disorders in
mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For
example, the nucleic acids (NCs) and vectors containing them and the PRO
polypeptide may be used to treat disorders associated with decreased PRO
expression. AAB77510 to AAB77721 and AAB244388 to AAB24435 represent
nucleotide and protein sequences used in the exemplification of the
present invention

XX Sequence 248 AA;

Query Match 100.0%; Score 248; DB 3; Length 248;

Best Local Similarity 100.0%; Pred. No. 8.4e-182;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGLSIFLLCVLGLSQAATPKIFNCTECGRNSQPMQVGLFECTSLRCGGVLIDHRWVLT 60

DB 1 MGLSIFLLCVLGLSQAATPKIFNCTECGRNSQPMQVGLFECTSLRCGGVLIDHRWVLT 60

OY 61 AHCSSRYVWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120

DB 61 AHCSSRYVWRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120

OY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180

DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180

OY 181 TSNMVCAGVPGQDACQDSGGPLVCGVLOGLVSGSVGPGQDGIPIGVYTYICKYVDW 240

DB 181 TSNMVCAGVPGQDACQDSGGPLVCGVLOGLVSGSVGPGQDGIPIGVYTYICKYVDW 240

OY 241 IRMIMRNN 248

DB 241 IRMIMRNN 248

RESULT 3

AAB24032

ID AAB24032 standard; protein; 248 AA.

XX AAB24032;

XX 25-JAN-2001 (first entry)

XX Human PRO1303 protein sequence SEQ ID NO:33.

XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
KW identification; tumourigenesis; anticancer; detection.

XX Homo sapiens.

XX WO200053750-A1.

XX 14-SEP-2000.

```

XX PF 02-DEC-1999; 99WO-US028551.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 01-SEP-1999; 99WO-US020111.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028634.
XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
XX
XX WPI; 2000-594320/56.
XX N-PSDB; AAC58114.
XX
XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
XX the growth of tumors in mammals; and to identify inhibitors of PRO
XX polypeptide activity or expression.
XX
XX Claim 61; Fig 24; 226pp; English.
XX
XX The present invention describes an antibody that binds to a human protein
XX (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
XX PRO1927; PRO3567; PRO1295; PRO1303; PRO4344; PRO4354; PRO4397;
XX PRO4407; PRO1555; PRO1096; PRO2038; and PRO2262. (I) has anticancer
XX activity and can be used to diagnose tumors in mammals, by detecting
XX complex formation when the antibody is contacted with test cells.
XX Increased expression of genes encoding (I) can also be detected to
XX diagnose tumors. Agents which inhibit the activity of (I), especially
XX the antibodies, or an antisense oligonucleotide which hybridises to genes
XX encoding (I), can be used to inhibit tumour growth, preferably by
XX inducing cell death. Methods from the present invention can be used to
XX identify compounds which inhibit the biological activity of (I). AAC58019
XX to AAC58102 represent PCR primers and hybridisation probes used in
XX examples from the present invention for human PRO sequences. AAC58103 to
XX AAC58122 and AAB24021 to AAB24040 represent human PRO polynucleotide and
XX protein sequences given in the exemplification of the present invention
XX
XX Sequence 248 AA;
XX
XX Query Match 100.0%; Score 248; DB 3; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-182;
XX Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
DB |||||||
DB 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
QY 61 AHCSGRYVRLGHELSLQDWTETQIRHSGFVTHPGYLCASTSHEHDLRLRLPVRV 120
DB |||||||
DB 61 AHCSGRYVRLGHELSLQDWTETQIRHSGFVTHPGYLCASTSHEHDLRLRLPVRV 120
QY 121 TSSVQPLPLPNDATAGTCHVSGWGITNHPRPFPDQLQCLNLSVSHATCHGVYPGRI 180
DB |||||||
DB 121 TSSVQPLPLPNDATAGTCHVSGWGITNHPRPFPDQLQCLNLSVSHATCHGVYPGRI 180
QY 181 TSNMVCAGVPQDQACQDSGGPLVCGVQLGVLVSWGSGVPCQDGIIPGVYTIICKYVDW 240
DB |||||||
DB 181 TSNMVCAGVPQDQACQDSGGPLVCGVQLGVLVSWGSGVPCQDGIIPGVYTIICKYVDW 240
QY 241 IRMIMRNN 248
DB |||||||
DB 241 IRMIMRNN 248
XX
XX RESULT 4
XX AA999393
XX ID AA999393 standard; protein; 248 AA.
XX
XX AC AA999393;
XX
XX DT 08-AUG-2000 (first entry)

```

```

XX DE Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
XX
XX KW Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
XX transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX
XX OS Homo sapiens.
XX
XX PN WO200012708-A2.
XX
XX PD 09-MAR-2000.
XX
XX PF 01-SEP-1999; 99WO-US020111.
XX
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 02-SEP-1998; 98US-0098936P.
XX 02-SEP-1998; 98US-0098959P.
XX 02-SEP-1998; 98US-0098960P.
XX 02-SEP-1998; 98US-0098964P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.
XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100384P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.
XX 16-SEP-1998; 98US-0100662P.
XX 16-SEP-1998; 98US-0100664P.
XX 17-SEP-1998; 98US-0100683P.
XX 17-SEP-1998; 98US-0100684P.
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XX 18-SEP-1998; 98US-0101279P.
XX 23-SEP-1998; 98US-0101471P.
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XX 23-SEP-1998; 98US-0101479P.
XX 24-SEP-1998; 98US-0101738P.
XX 24-SEP-1998; 98US-0101741P.
XX 24-SEP-1998; 98US-0101743P.
XX 24-SEP-1998; 98US-0101915P.
XX 24-SEP-1998; 98US-0101916P.
XX 29-SEP-1998; 98US-0102207P.
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XX 29-SEP-1998; 98US-0102307P.
XX 29-SEP-1998; 98US-0102331P.
XX 29-SEP-1998; 98US-0102331P.
XX 30-SEP-1998; 98US-0102484P.
XX 30-SEP-1998; 98US-0102487P.
XX 30-SEP-1998; 98US-0102570P.

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 PR 01-OCT-1998; 98US-0102687P.
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 PR 06-OCT-1998; 98US-0103258P.
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 PR 07-OCT-1998; 98US-0103314P.
 PR 07-OCT-1998; 98US-0103315P.
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 PR 07-OCT-1998; 98US-0103395P.
 PR 07-OCT-1998; 98US-0103396P.
 PR 07-OCT-1998; 98US-0103401P.
 PR 08-OCT-1998; 98US-0103633P.
 PR 08-OCT-1998; 98US-0103678P.
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 PR 14-OCT-1998; 98US-0104257P.
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 PR 20-OCT-1998; 98US-0105000P.
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 PR 26-OCT-1998; 98US-0105693P.
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 PR 29-OCT-1998; 98US-0106248P.
 PR 29-OCT-1998; 98US-0106384P.
 PR 29-OCT-1998; 98US-0108500P.
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 PR 03-NOV-1998; 98US-0106902P.
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 PR 03-NOV-1998; 98US-0106934P.
 PR 10-NOV-1998; 98US-0107783P.
 PR 17-NOV-1998; 98US-0108775P.
 PR 17-NOV-1998; 98US-0108779P.
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 PR 17-NOV-1998; 98US-0108801P.
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 PR 17-NOV-1998; 98US-0108806P.
 PR 17-NOV-1998; 98US-0108807P.
 PR 17-NOV-1998; 98US-0108867P.
 PR 17-NOV-1998; 98US-0108925P.
 PR 18-NOV-1998; 98US-0108848P.
 PR 18-NOV-1998; 98US-0108849P.
 PR 18-NOV-1998; 98US-0108850P.
 PR 18-NOV-1998; 98US-0108851P.
 PR 18-NOV-1998; 98US-0108852P.
 PR 18-NOV-1998; 98US-0108858P.
 PR 18-NOV-1998; 98US-0108904P.
 PR XX (GETH) GENENTECH INC.
 PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
 PI WPI; 2000-237871/20.
 DR N-PSDB; AAA37075.
 XX New mammalian DNA sequences encoding transmembrane, receptor or secreted
 PT PRO polypeptides, useful for screening of potential peptide or small

PT molecule inhibitors of the relevant receptor/ligand interactions.
 XX Claim 12; Fig 108; 773pp; English.
 XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
 CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
 CC transmembrane and receptor PRO proteins can be used for screening of
 CC potential peptide or small molecule inhibitors of the relevant
 CC receptor/ligand interactions. The polypeptides and nucleotide sequences
 CC encoding then have various industrial applications, including uses as
 CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
 CC primers and hybridisation probes used in the isolation of the PRO
 CC polypeptides from the present invention
 XX Sequence 248 AA;
 SQ

Query Match 100.0%; Score 248; DB 3; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGLSIFLLLCVLGLSQATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWVLT A 60
 Db 1 MGLSIFLLLCVLGLSQATPKIFNGTECGRNQPMQVGLFEGTSLRCGGVLIDHRWVLT A 60
 QY 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGSPVTHGYLGASTSHSHDLRLRLPVRV 120
 Db 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGSPVTHGYLGASTSHSHDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPDPDLQLCLNLSIVSHATCHGVVPGRI 180
 Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPDPDLQLCLNLSIVSHATCHGVVPGRI 180
 QY 181 TSNMVCAGVPGQDACQGDGSGGLVCGGVLCGLVSGVSGPCQDGI PGVYTYICKYVDW 240
 Db 181 TSNMVCAGVPGQDACQGDGSGGLVCGGVLCGLVSGVSGPCQDGI PGVYTYICKYVDW 240
 QY 241 IRMIMRNN 248
 Db 241 IRMIMRNN 248

RESULT 5
 AAM23994
 ID AAM23994 standard; protein; 248 AA.
 XX AC AAM23994;
 XX DT 12-OCT-2001 (first entry)
 XX DE Human EST encoded protein SEQ ID NO: 1519.
 XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostic; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 XX OS Homo sapiens.
 XX WO200154477-A2.
 XX PN 02-AUG-2001.
 XX PF 25-JAN-2001; 2001WO-US002687.
 XX PR 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.
DR N-PSDB; AAH98653.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 1048-1049; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 248; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLPFGTSLRCGVLIDHRWVLT 60
Db 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLPFGTSLRCGVLIDHRWVLT 60
Qy 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Db 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
Qy 181 TSNMVCAGGVPGQDACQDGSGLVCGVGLQGLVSGVSGPGQDGPVGYTYICKYVDM 240
Db 181 TSNMVCAGGVPGQDACQDGSGLVCGVGLQGLVSGVSGPGQDGPVGYTYICKYVDM 240
Qy 241 IRMTMRNN 248
Db 241 IRMTMRNN 248
RESULT 6
AAB66142
ID AAB66142 standard; protein; 248 AA.
XX
AC AAB66142;
XX
DT 02-APR-2001 (first entry)
XX
DE Protein of the invention #54.
XX
KW Secreted; transmembrane; gene therapy.
XX
OS Unidentified.
XX
FN WO200078961-A1.
XX
PD 28-DEC-2000.
XX
PF 18-FEB-2000; 2000WO-US004342.
XX
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Botstein D, Deenoyers L, Eaton DL, Ferrara N, Fong SJ,
PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams FM, Wood WI;
XX
XX WPI; 2001-071395/08.
XX
XX Secreted and transmembrane proteins and nucleic acids designated PRO,
XX useful as hybridization probes, in chromosome and gene mapping and gene
XX therapy.
XX
PS Claim 1; Fig 108; 787pp; English.
XX
CC The present invention relates to secreted and transmembrane proteins.
CC These proteins and the DNA encoding them may be used as hybridization
CC probes, in chromosome and gene mapping and in the generation of anti-
CC sense RNA and DNA. They may also be used to generate either
CC transgenic animals or knockout animals which are in turn useful for
CC development and screening of therapeutically useful reagents. The nucleic
CC acids may also be used in gene therapy
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 248; DB 4; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLPFGTSLRCGVLIDHRWVLT 60
Db 1 MGLSIFLLLCVGLSQAATPKIFNGTECGRNSQPMQVGLPFGTSLRCGVLIDHRWVLT 60
Qy 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Db 61 AHCSGSRYWVRLGHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRV 120
Qy 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
Qy 181 TSNMVCAGGVPGQDACQDGSGLVCGVGLQGLVSGVSGPGQDGPVGYTYICKYVDM 240
Db 181 TSNMVCAGGVPGQDACQDGSGLVCGVGLQGLVSGVSGPGQDGPVGYTYICKYVDM 240
Qy 241 IRMTMRNN 248
Db 241 IRMTMRNN 248
RESULT 7
ABO33635
ID ABO33635 standard; protein; 248 AA.
XX
AC ABO33635;
XX
XX 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1303.
XX
KW Human; secreted and transmembrane protein; PRO; angiogenesis;
KW endothelial cell proliferation; wound healing; immune response;
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;
KW cardiac insufficiency disorder; calcium flux; inflammation;
KW vascular endothelial growth factor-stimulated proliferation;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;
KW pancreatic beta-cell precursor cell differentiation; thalassemias;
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;

cartilage disorder; sports injury; arthritis.

Homo sapiens.

US2003073130-A1.

17-APR-2003.

11-DEC-2001; 2001US-00015869.

01-SEP-1998; 98US-0098716P.

01-SEP-1998; 98US-0098723P.

01-SEP-1998; 98US-0098749P.

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02-SEP-1998; 98US-0098803P.

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17-SEP-1998; 98US-0100684P.

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24-SEP-1998; 98US-0101916P.

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06-OCT-1998; 98US-0103258P.

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26-OCT-1998; 98US-0105694P.

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28-OCT-1998; 98US-0106023P.

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28-OCT-1998; 98US-0106032P.

28-OCT-1998; 98US-0106033P.

28-OCT-1998; 98US-0106178P.

29-OCT-1998; 98US-0106248P.

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29-OCT-1998; 98US-0108500P.

30-OCT-1998; 98US-0106464P.

03-NOV-1998; 98US-0106856P.

03-NOV-1998; 98US-0106902P.

03-NOV-1998; 98US-0106905P.

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10-NOV-1998; 98US-0107783P.

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17-NOV-1998; 98US-0108787P.

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17-NOV-1998; 98US-0108802P.

17-NOV-1998; 98US-0108806P.

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17-NOV-1998; 98US-0108925P.

18-NOV-1998; 98US-0108848P.

18-NOV-1998; 98US-0108849P.

18-NOV-1998; 98US-0108850P.

18-NOV-1998; 98US-0108851P.

18-NOV-1998; 98US-0108852P.

18-NOV-1998; 98US-0108858P.

18-NOV-1998; 98US-0108904P.

22-DEC-1998; 98US-0113296P.

30-DEC-1998; 98US-0114223P.

05-JAN-1999; 99WO-US000106.

16-APR-1999; 99US-0129674P.

23-JUN-1999; 99US-0141037P.

20-JUL-1999; 99US-0144758P.

26-JUL-1999; 99US-0145698P.

01-SEP-1999; 99WO-US020111.

15-SEP-1999; 99WO-US021194.

29-OCT-1999; 99US-0162505P.

30-NOV-1999; 99WO-US028313.

02-DEC-1999; 99WO-US028551.

16-DEC-1999; 99WO-US030095.

05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US0003565.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 28-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023322.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 28-JUN-2001; 2001WO-US019592.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 04-SEP-2001; 2001US-00946374.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
 PI Williams PM, Wood WI;
 XX WPI; 2003-585293/55.
 DR N-PSDB; ACD68378.
 XX Novel isolated PRO polypeptides e.g. PRO1130, PRO1275, PRO1418, PRO1555,
 PT PRO1787 that modulate glucose or free fatty acid uptake by skeletal
 PT muscle cells, and are useful for treating diabetes, hyper- or hypo-

Query Match 100.0%; Score 248; DB 6; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.4e-182;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVGLSQATPKIFNGTECGNSOPWQVGLFEGTSLRCGGVLIDHRWLTA 60
 DB 1 MGLSIFLLLCVGLSQATPKIFNGTECGNSOPWQVGLFEGTSLRCGGVLIDHRWLTA 60
 QY 61 AHCSGRYWRLEHSLQDWTQIRHSGFSVTHPGYLCASTSHEHDLRLRLPVRV 120
 DB 61 AHCSGRYWRLEHSLQDWTQIRHSGFSVTHPGYLCASTSHEHDLRLRLPVRV 120
 QY 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDQLQLNLSIVSHATCHGVYPGR 180
 DB 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPNPPDQLQLNLSIVSHATCHGVYPGR 180
 QY 181 TSNMVCAGGVPGDAGCGSGGLVCGGVLCGLVSGVSGVPCQDGIPIGVYTI CKYVDW 240
 DB 181 TSNMVCAGGVPGDAGCGSGGLVCGGVLCGLVSGVSGVPCQDGIPIGVYTI CKYVDW 240
 QY 241 IRIMERNN 248
 DB 241 IRIMERNN 248

RESULT 8
 ID ABO44488
 XX ABO44488 standard; protein; 248 AA.
 AC ABO44488;
 XX 01-OCT-2003 (first entry)
 DT Human secreted/transmembrane protein PRO1303.
 DE Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;
 XX Human; secreted protein; transmembrane protein; PRO; vulnery; cardiant;

KW antidiabetic; anorectic; antiarthritic; angiogenesis; cancer;
 KW adrenal cortical capillary; endothelial cell growth; wound healing;
 KW stimulated T-lymphocyte proliferation; immune response suppression;
 KW neonatal heart hypertrophy; cardiac insufficiency disorder;
 KW vascular endothelial growth factor; inflammation; mononuclear cell;
 KW eosinophil; diabetes; obesity; or hyper-insulinaemia; hypo-insulinaemia;
 KW chondrocyte redifferentiation; bone disorder; cartilage disorder;
 KW sports injury; arthritis.
 XX Homo sapiens.
 XX US2003044841-A1.
 XX 06-MAR-2003.
 XX 06-DEC-2001; 2001US-00006856.
 PR 01-SEP-1998; 98US-0098716P.
 PR 01-SEP-1998; 98US-0098723P.
 PR 01-SEP-1998; 98US-0098749P.
 PR 02-SEP-1998; 98US-0098750P.
 PR 02-SEP-1998; 98US-0098803P.
 PR 02-SEP-1998; 98US-0098821P.
 PR 02-SEP-1998; 98US-0098843P.
 PR 09-SEP-1998; 98US-0099536P.
 PR 09-SEP-1998; 98US-0099596P.
 PR 09-SEP-1998; 98US-0099598P.
 PR 09-SEP-1998; 98US-0099602P.
 PR 09-SEP-1998; 98US-0099642P.
 PR 10-SEP-1998; 98US-0099741P.
 PR 10-SEP-1998; 98US-0099754P.
 PR 10-SEP-1998; 98US-0099763P.
 PR 10-SEP-1998; 98US-0099792P.
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 PR 29-SEP-1998; 98US-0102240P.
 PR 29-SEP-1998; 98US-0102307P.
 PR 29-SEP-1998; 98US-0102330P.

ID ABO3J512 standard; protein; 248 AA.
XX ABO3J512;
DT XX
TT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1303.
XX
KW Human; secreted and transmembrane protein; PRO; gene therapy; vaccine;
KW tissue typing; chromosome identification; vaccine.
XX
OS Homo sapiens.
XX
PN US2003073129-A1.
XX
PD 17-APR-2003.
XX
XX 04-SEP-2001; 2001US-00946374.
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PR 01-SEP-1998; 98US-0098716P.
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PR 26-OCT-1998; 98US-0105693P.
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PR 28-OCT-1998; 98US-0106178P.
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PR 30-OCT-1998; 98US-0106464P.
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PR 03-NOV-1998; 98US-0106905P.
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PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
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PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
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PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 22-DEC-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-00218517.
PR 30-DEC-1998; 98US-0113296P.
PR 03-JAN-1999; 98US-0114223P.
PR 99WO-US000106.

PR 12-APR-1999; 99US-00284291.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 18-OCT-1999; 99US-00403297.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 22-MAY-2000; 2000WO-US013705.
PR 17-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023532.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PA (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
XX Gao W, Goddard A, Godowski FJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WT;
XX WPI; 2003-585292/55.
DR N-PSDB; ACD68024.
XX
XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the
PT preparation of a medicament for treating a condition responsive to PRO
PT polypeptide, and as therapeutic agents e.g. vaccines.
PS Claim 12; Fig 108; 561pp; English.
XX
XX The invention describes an isolated PRO (secreted and transmembrane)
CC polypeptide (1), having at least 80% sequence identity to a sequence
Query Match 100.0%; Score 248; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGSLFLLLCVLGLSQATPKLFGNTECGRNSQPMQVGLFECTSLRCGVLIDHRWLTA 60
DB 1 MGSLFLLLCVLGLSQATPKLFGNTECGRNSQPMQVGLFECTSLRCGVLIDHRWLTA 60
QY 61 AHCSGSRYWVRIGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEDLRLRLPLVRV 120
DB 61 AHCSGSRYWVRIGHSLSQLDWTEQIRHSGFVTHPGYLGASTSHEDLRLRLPLVRV 120
QY 121 TSSVQPLPLPNDCATAGTCHVSGWGITNHPNPPDLLLQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVQPLPLPNDCATAGTCHVSGWGITNHPNPPDLLLQCLNLSIVSHATCHGVYPGRI 180
QY 181 TSNMVCAGVPQDACCQDSGGLVCGPLVCGVQLQGLVSGVSGPGQDGIPOGVYTYICKYVDW 240
DB 181 TSNMVCAGVPQDACCQDSGGLVCGPLVCGVQLQGLVSGVSGPGQDGIPOGVYTYICKYVDW 240

Db 181 TSNMVCAGVPQDACCQDSGGLVCGPLVCGVQLQGLVSGVSGPGQDGIPOGVYTYICKYVDW 240
QY 241 IRIMIRNN 248
DB 241 IRIMIRNN 248
RESULT 10
ADCI8063
ID ADCI8063 standard; protein; 248 AA.
AC ADCI8063;
XX 18-DEC-2003 (first entry)
DE Human PRO polypeptide #54.
XX Human; PRO; protein electrophoresis; chromosome mapping; gene mapping;
genetic disorder.
OS Homo sapiens.
XX US2003064925-A1.
PN 03-APR-2003.
XX 10-DEC-2001; 2001US-00013907.
XX 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
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PR 10-SEP-1998; 98US-0099763P.
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PR 10-SEP-1998; 98US-0099816P.
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PR 15-SEP-1998; 98US-0100388P.
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PR	06-OCT-1998;	98US-0103258P.	PR	06-JAN-2000;	2000WO-US000376.
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PR	08-OCT-1998;	98US-0103679P.	PR	23-AUG-2000;	2000WO-US023522.
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PR	20-OCT-1998;	98US-0105000P.	PR	10-NOV-2000;	2000WO-US030873.
PR	20-OCT-1998;	98US-0105002P.	PR	01-DEC-2000;	2000WO-US032678.
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PR	21-OCT-1998;	98US-0105169P.	PR	01-MAR-2001;	2001WO-US006666.
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PR	26-OCT-1998;	98US-0105694P.	PR	29-JUN-2001;	2001WO-US021066.
PR	27-OCT-1998;	98US-0105807P.	PR	09-JUL-2001;	2001WO-US021735.
PR	27-OCT-1998;	98US-0105881P.	PR	04-SEP-2001;	2001US-00946374.
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PR	27-OCT-1998;	98US-0106062P.	XX		
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PR	28-OCT-1998;	98US-0106030P.	PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;	
PR	28-OCT-1998;	98US-0106032P.	PI	Williams PW, Wood WI;	
PR	28-OCT-1998;	98US-0106033P.	XX	WPI; 2003-555602/52.	
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PR	29-OCT-1998;	98US-0106384P.	XX		
PR	29-OCT-1998;	98US-0108500P.	PT	Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the	
PR	30-OCT-1998;	98US-0106464P.	PT	preparation of a medicament for treating a condition responsive to PRO	
PR	03-NOV-1998;	98US-0106856P.	PT	polypeptide, and as therapeutic agents e.g. vaccines.	
PR	03-NOV-1998;	98US-0106902P.	XX	Claim 12; SEQ ID NO 194; 555pp; English.	
PR	03-NOV-1998;	98US-0106905P.	PS	The invention relates to human PRO polypeptides and the polynucleotides	
PR	03-NOV-1998;	98US-0106919P.	XX	encoding them. The sequences are useful in the preparation of a	
PR	03-NOV-1998;	98US-0106932P.	CC	medicament for treating a condition responsive to a PRO polypeptide. The	
PR	10-NOV-1998;	98US-0107783P.	CC	polypeptides are useful in a number of functional biological assays, as	
PR	17-NOV-1998;	98US-0108775P.	CC	molecular weight markers for protein electrophoresis and as therapeutic	
PR	17-NOV-1998;	98US-0108779P.			
PR	17-NOV-1998;	98US-0108787P.			
PR	17-NOV-1998;	98US-0108788P.			
PR	17-NOV-1998;	98US-0108801P.			
PR	17-NOV-1998;	98US-0108802P.			
PR	17-NOV-1998;	98US-0108806P.			
PR	17-NOV-1998;	98US-0108807P.			
PR	17-NOV-1998;	98US-0108867P.			
PR	17-NOV-1998;	98US-0108925P.			
PR	18-NOV-1998;	98US-0108848P.			
PR	18-NOV-1998;	98US-0108849P.			
					Query Match 100.0%; Score 248; DB 7; Length 248;
					Best Local Similarity 100.0%; Pred. No. 8.4e-182; Indels 0; Gaps 0;
					Matches 248; Conservative 0; Mismatches 0;
QY	1	MGLSIFLLLCVLGLSQATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT	60		
DB	1	MGLSIFLLLCVLGLSQATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWVLT	60		
QY	61	AHCSGRYVWRLGHEHLSQLDWTQTRHSQFSVTHPGYLGASTSHEHDLRLRLPRV	120		

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Qy 121 TSSVQPLPLNDCATAGTECHVSGWGI TNHPRNPDPDLLOCLNLSIVSHATCHGVYPCR I 180
Db 121 TSSVQPLPLNDCATAGTECHVSGWGI TNHPRNPDPDLLOCLNLSIVSHATCHGVYPCR I 180
Qy 181 TSNMVCAGVPGQDACQCGDSGGLVCGGVLAGLWSGVSVPQGDGIFGVYTYICKYVDW 240
Db 181 TSNMVCAGVPGQDACQCGDSGGLVCGGVLAGLWSGVSVPQGDGIFGVYTYICKYVDW 240
Qy 241 IRMINRNN 248
Db 241 IRMINRNN 248

RESULT 11
ADD70709
ID ADD70709 standard; protein; 248 AA.
XX AC ADD70709;
XX DT 15-JAN-2004 (first entry)
XX DE Human secreted/transmembrane protein PRO1303.
XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
XX KW immune response; cardiac insufficiency disorder; calcium flux;
XX KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
XX KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
XX KW dermatitis; herpetiformis; Crohn's disease; thalassaemia.
XX OS Homo sapiens.
XX FN US2003099625-A1.
XX PD 29-MAY-2003.
XX PF 12-DEC-2001; 2001US-00015386.
XX PR 01-SEP-1998; 98US-0098716P.
XX PR 01-SEP-1998; 98US-0098723P.
XX PR 01-SEP-1998; 98US-0098749P.
XX PR 01-SEP-1998; 98US-0098750P.
XX PR 02-SEP-1998; 98US-0098803P.
XX PR 02-SEP-1998; 98US-0098821P.
XX PR 02-SEP-1998; 98US-0098843P.
XX PR 02-SEP-1998; 98US-0099536P.
XX PR 09-SEP-1998; 98US-0099596P.
XX PR 09-SEP-1998; 98US-0099598P.
XX PR 09-SEP-1998; 98US-0099602P.
XX PR 09-SEP-1998; 98US-0099642P.
XX PR 10-SEP-1998; 98US-0099741P.
XX PR 10-SEP-1998; 98US-0099754P.
XX PR 10-SEP-1998; 98US-0099763P.
XX PR 10-SEP-1998; 98US-0099792P.
XX PR 10-SEP-1998; 98US-0099808P.
XX PR 10-SEP-1998; 98US-0099812P.
XX PR 10-SEP-1998; 98US-0099815P.
XX PR 10-SEP-1998; 98US-0099816P.
XX PR 15-SEP-1998; 98US-0100385P.
XX PR 15-SEP-1998; 98US-0100388P.
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XX PR 16-SEP-1998; 98US-0100584P.
XX PR 16-SEP-1998; 98US-0100627P.
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PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
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PR 24-SEP-1998; 98US-0101916P.
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PR 21-OCT-1998; 98US-0105104P.
PR 22-OCT-1998; 98US-0105169P.
PR 22-OCT-1998; 98US-0105266P.
PR 26-OCT-1998; 98US-0105693P.
PR 26-OCT-1998; 98US-0105694P.
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PR 28-OCT-1998; 98US-0106023P.
PR 28-OCT-1998; 98US-0106029P.
PR 28-OCT-1998; 98US-0106030P.
PR 28-OCT-1998; 98US-0106032P.
PR 28-OCT-1998; 98US-0106033P.
PR 28-OCT-1998; 98US-0106178P.
PR 29-OCT-1998; 98US-0106248P.
PR 29-OCT-1998; 98US-0106384P.
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PR 03-NOV-1998; 98US-0106856P.
PR 03-NOV-1998; 98US-0106902P.
PR 03-NOV-1998; 98US-0106905P.
PR 03-NOV-1998; 98US-0106919P.
PR 03-NOV-1998; 98US-0106932P.
PR 03-NOV-1998; 98US-0106934P.
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PR 10-NOV-1998; 98US-0107783P.
PR 17-NOV-1998; 98US-0108775P.
PR 17-NOV-1998; 98US-0108779P.
PR 17-NOV-1998; 98US-0108787P.
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PR 17-NOV-1998; 98US-0108806P.
PR 17-NOV-1998; 98US-0108807P.
PR 17-NOV-1998; 98US-0108867P.
PR 17-NOV-1998; 98US-0108925P.
PR 18-NOV-1998; 98US-0108848P.
PR 18-NOV-1998; 98US-0108849P.
PR 18-NOV-1998; 98US-0108850P.
PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR 22-DEC-1998; 98US-0113286P.
PR 30-DEC-1998; 98US-0114223P.
PR 05-JAN-1999; 99WO-US000106.
PR 16-APR-1999; 99US-0129674P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006520.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US030873.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX (GETH ) GENENTECH INC.
PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-874602/81.
DR N-PSDB; ADD70708.
XX
XX Novel isolated PRO polypeptides e.g., PRO1130, PRO1275, PRO1418, PRO1555,
PT PRO1787 affect glucose or free fatty acid (FFA) uptake by skeletal muscle
PT cells and are useful for treating diabetes or hyper- or hypo-insulinemia.
XX
XX Claim 12; SEQ ID NO 194; 553pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
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Query Match 100.0%; Score 248; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 0;

QY 1 MGLSIFLLLCVLCGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60
DB 1 MGLSIFLLLCVLCGLSQAATPKIFNGTECGRNSQPMQVGLFEGTSLRCGGVLIDHRWLTA 60

QY 61 AHCSGSRYVVRVLRGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPRV 120
DB 61 AHCSGSRYVVRVLRGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPRV 120

QY 121 TSSVQPLPLPNDCAATAGTECHSGMGTNNHPRPPDQLCLNLSIVSHATCHGVYPERI 180
DB 121 TSSVQPLPLPNDCAATAGTECHSGMGTNNHPRPPDQLCLNLSIVSHATCHGVYPERI 180

QY 181 TSNMVCAGVPGQDACQSGDGLVCGGVLCGLVSGSVGPGQDGIPIGVYTYICKYVDW 240
DB 181 TSNMVCAGVPGQDACQSGDGLVCGGVLCGLVSGSVGPGQDGIPIGVYTYICKYVDW 240

QY 241 IRMIMENN 248
DB 241 IRMIMENN 248

RESULT 12
ADD39786
ID ADD39786 standard; protein; 248 AA.
XX AC ADD39786;
XX DT 15-JAN-2004 (first entry)
XX DB Human secreted/transmembrane protein PRO1303.
XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schönlain-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX OS Homo sapiens.
XX PN US2003083462-A1.
XX PD 01-MAY-2003.
XX PF 10-DEC-2001; 2001US-00013913.
XX PR 05-JAN-1999; 99WO-US000106.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021194.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006520.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US030873.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
XX

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PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK;
PI Williams PM, Wood WI;
XX
XX WPI; 2003-755122/71.
DR N-PSDB; ADD39785.
XX
XX New secreted and transmembrane PRO polypeptides useful for treating
PT cancers, kidney disorders, Crohn's disease, diabetes mellitus, hyper- or
PT hypo-insulinemia, sports injuries and arthritis.
XX
XX Claim 12; SEQ ID NO 194; 557bp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity
CC to an amino acid sequence chosen from 123 fully defined sequences as
CC given in the specification (including their extracellular domains either
CC or without their associated signal peptides. Also include are the
CC nucleotide (NA) sequences encoding PRO, a vector comprising the PRO NA, a
CC host cell comprising the vector, producing PRO, a chimeraic molecule
CC comprising PRO fused to a heterologous amino acid sequence, and an anti-
CC PRO antibody. PRO is useful as molecular weight markers for protein
CC electrophoresis and also for chromosome identification. PRO is also
CC useful for tissue typing. PRO and PRO NA are useful as hybridisation
CC probes for a cDNA library to isolate the full-length PRO cDNA. PRO NA is
CC useful for generating transgenic animals or knock-out animals which are
CC useful in development and screening useful reagents. PRO NA is also
CC useful in gene therapy. PRO1244, PRO1286 and PRO1303 polypeptides are
CC useful for treating cancerous tumours. PRO1250, PRO1418 and PRO1410
CC polypeptides are useful for suppressing immune response. PRO1246
CC polypeptide is useful for treating cardiac insufficiency disorders.
CC PRO1246 polypeptide is also useful for treating tumours PRO1246 and
CC PRO1561 polypeptide are useful for stimulating calcium flux in human
CC umbilical vein endothelial cells. PRO1265, PRO1250 and PRO1474
CC polypeptides are useful for treating bone and/or cartilage disorders
CC (e.g. arthritis) and wound healing. PRO1130, PRO1275 and PRO1418
CC polypeptides are useful for treating diabetes in skeletal muscle cells
CC and obesity. PRO1265, PRO1244 and PRO1382 polypeptides are useful for
CC treating Berger disease or other nephropathies associated with Schonlein-
CC Henoch purpura, coeliac disease, dermatitis, herpeticiformis or Crohn's
CC disease. PRO1478, PRO1265, PRO1412, PRO1279, PRO1304, PRO1306, PRO1418,
CC PRO1410 and PRO1575 are useful in treating thalassaemias. The present
CC sequence represents a PRO protein of the invention.
XX
SQ Sequence 248 AA;
Query Match 100.0%; Score 248; DB 7; Length 248;
Beet Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPQVGLFEGTSLRCGVLIHWRVLT 60
Db 1 MGLSIFLLCVLGLSQAATPKIFNGTECGRNSQPQVGLFEGTSLRCGVLIHWRVLT 60
Oy 61 AHCSGSRVWVPLGEHSLSQLDWTOIRHSGSVTHPGVLGASTSHEHDLRLRLPVRV 120
Db 61 AHCSGSRVWVPLGEHSLSQLDWTOIRHSGSVTHPGVLGASTSHEHDLRLRLPVRV 120
Oy 121 TSSVQPLPLPNDCATAGTECHVSGWGIINHPNPFPPDLLQCLNLSIVSHATCHGVYPCR 180
Db 121 TSSVQPLPLPNDCATAGTECHVSGWGIINHPNPFPPDLLQCLNLSIVSHATCHGVYPCR 180
Oy 181 TSNMVCAGGVPGQDACQCGSDGGLVCGGVLGGLVSMGSGVPGCGDGIPIGVVYICKYVDM 240
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Db 181 TSNMVCAGGVPGQDACQCGSDGGLVCGGVLGGLVSMGSGVPGCGDGIPIGVVYICKYVDM 240
Oy 241 IRMIMRNN 248
Db 241 IRMIMRNN 248
RESULT 13
ADD70232
ID ADD70232 standard; protein; 248 AA.
XX
AC ADD70232;
XX
XX 15-JAN-2004 (first entry)
XX Human secreted/transmembrane protein PRO1303.
XX
XX Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX
XX Homo sapiens.
XX
XX US2003054406-A1.
XX
XX 20-MAR-2003.
XX
XX 06-DEC-2001; 2001US-00006818.
XX
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
XX 02-SEP-1998; 98US-0098821P.
XX 02-SEP-1998; 98US-0098843P.
XX 02-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
XX 09-SEP-1998; 98US-0099598P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
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XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
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XX 16-SEP-1998; 98US-0100664P.
XX 17-SEP-1998; 98US-0100683P.
XX 17-SEP-1998; 98US-0100684P.
XX 17-SEP-1998; 98US-0100710P.
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XX 17-SEP-1998; 98US-0100930P.
XX 18-SEP-1998; 98US-0100848P.
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XX 18-SEP-1998; 98US-0101014P.
XX 18-SEP-1998; 98US-0101068P.
XX 18-SEP-1998; 98US-0101071P.
XX 22-SEP-1998; 98US-0101275P.
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DB 61 AHCSRYVRLGHSLSOLDWTEQIRHSQFSTHRCYLGASTSHHDLRLRLPVRV 120
QY 121 TSSVOPLPNDCATAGTCHVSGWGTNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
DB 121 TSSVOPLPNDCATAGTCHVSGWGTNHPNPPDLLQCLNLSIVSHATCHGVYPGRI 180
QY 181 TSNMVCAGVPGQDACQGDGSGPLVCGGVLOGLVSGSVGPGQDGIPIGVYTYICKYVDW 240
DB 181 TSNMVCAGVPGQDACQGDGSGPLVCGGVLOGLVSGSVGPGQDGIPIGVYTYICKYVDW 240
QY 241 IRMIMRN 248
DB 241 IRMIMRN 248

RESULT 14
ADD38353
ID ADD38353 standard; protein; 248 AA.
XX AC
XX ADD38353;
XX XX
DT 15-JAN-2004 (first entry)
XX XX
DE Human secreted/transmembrane protein PRO1303.
XX Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassaemia.
XX Homo sapiens.
QS OS
XX US2003096955-A1.
XX FN
XX PD
XX 22-MAY-2003.
XX XX
XX 07-DEC-2001; 2001US-00012755.
XX XX
XX 01-SEP-1998; 98US-0098716P.
XX 01-SEP-1998; 98US-0098723P.
XX 01-SEP-1998; 98US-0098749P.
XX 01-SEP-1998; 98US-0098750P.
XX 02-SEP-1998; 98US-0098803P.
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XX 02-SEP-1998; 98US-0098843P.
XX 09-SEP-1998; 98US-0099536P.
XX 09-SEP-1998; 98US-0099596P.
XX 09-SEP-1998; 98US-0099598P.
XX 09-SEP-1998; 98US-0099602P.
XX 09-SEP-1998; 98US-0099642P.
XX 10-SEP-1998; 98US-0099741P.
XX 10-SEP-1998; 98US-0099754P.
XX 10-SEP-1998; 98US-0099763P.
XX 10-SEP-1998; 98US-0099792P.
XX 10-SEP-1998; 98US-0099808P.
XX 10-SEP-1998; 98US-0099812P.
XX 10-SEP-1998; 98US-0099815P.
XX 10-SEP-1998; 98US-0099816P.
XX 15-SEP-1998; 98US-0100385P.
XX 15-SEP-1998; 98US-0100388P.
XX 15-SEP-1998; 98US-0100390P.
XX 16-SEP-1998; 98US-0100584P.
XX 16-SEP-1998; 98US-0100627P.
XX 16-SEP-1998; 98US-0100661P.
XX 16-SEP-1998; 98US-0100662P.
XX 16-SEP-1998; 98US-0100664P.
XX 17-SEP-1998; 98US-0100683P.
XX 17-SEP-1998; 98US-0100684P.
XX 17-SEP-1998; 98US-0100710P.
XX 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101915P.
PR 24-SEP-1998; 98US-0101916P.
PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
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PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102484P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
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PR 02-OCT-1998; 98US-0102687P.
PR 06-OCT-1998; 98US-0102963P.
PR 06-OCT-1998; 98US-0103258P.
PR 07-OCT-1998; 98US-0103449P.
PR 07-OCT-1998; 98US-0103314P.
PR 07-OCT-1998; 98US-0103315P.
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PR 16-APR-1999; 99US-0129674P.
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PR 26-JUL-1999; 99US-0145698P.
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PR 02-DEC-1999; 99WO-US028551.
PR 16-DEC-1999; 99WO-US030095.
PR 05-JAN-2000; 2000WO-US000219.
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PR 11-FEB-2000; 2000WO-US003565.
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PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
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PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 24-AUG-2000; 2000WO-US023328.
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PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.
XX
PA (GETH) GENENTECH INC.
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NP, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams FW, Wood WI;
XX
XX WPI; 2003-787000/74.
DR N-PSDB; ADD38352.
XX
XX Novel isolated PRO polypeptide, useful for treating cancerous tumors,
PT cardiac insufficiency disorders, wound healing, diabetes mellitus,
PT thalassemias.
XX
PS Claim 12; SEQ ID NO 194; 556pp; English.
XX
XX The invention relates to an isolated PRO polypeptide (secreted or
CC transmembrane protein) having at least 80% amino acid sequence identity

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Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX AC ADD39309;
XX DT 15-JAN-2004 (first entry)
XX DE Human secreted/transmembrane protein PRO1303.
XX KW Human; secreted protein; transmembrane protein; PRO; tumour;
KW immune response; cardiac insufficiency disorder; calcium flux;
KW umbilical vein endothelial cell; bone disorder; cartilage disorder;
KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;
KW Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;
KW dermatitis; herpeticiformis; Crohn's disease; thalassemia.
XX OS Homo sapiens.
XX PN US2003096954-A1.
XX PD 22-MAY-2003.
XX PF 07-DEC-2001; 2001US-00011671.
XX PR 01-SEP-1998; 98US-0098716P.
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PR 29-OCT-1998; 98US-0106248P.
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PR 30-OCT-1998; 98US-0106464P.
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PR 16-DEC-1999; 99WO-US030095.
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PR 01-MAR-2001; 2001WO-US006666.
PR 01-JUN-2001; 2001WO-US017800.
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PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 04-SEP-2001; 2001US-00946374.

(GETH) GENENTECH INC.

PA Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;
PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;
PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;
PI Williams PM, Wood WI;
XX WPI; 2003-786999/74.

DR N-PSDB; ADD39308.
XX Novel isolated PRO polypeptide useful for tissue typing, modulating
PT biological activity of cell, as molecular weight markers in protein
PT electrophoresis, for treating arthritis, tumor.
XX
PS Claim 12; SEQ ID NO 194; 550pp; English.
XX
CC The invention relates to an isolated PRO polypeptide (secreted or
Query Match 100.0%; Score 248; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 8.4e-182;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 IRMIMRNN 248

Search completed: June 16, 2004, 15:13:31
Job time : 61 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 16, 2004, 15:11:22 ; Search time 21 Seconds
(without alignments)
1135.976 Million cell updates/sec

Title: US-10-006-116A-194
Perfect score: 248
Sequence: 1 MGLSIFLLCVLGLSQARP.....GVYTYICKYVDIMRMIRNN 248

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	13	5.2	246	1 DBHU	complement factor
2	13	5.2	394	2 JS0600	t-plasminogen acti
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6	13	5.2	477	2 JS0598	t-plasminogen acti
7	13	5.2	559	1 A35029	t-plasminogen acti
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9	13	5.2	562	1 UKHUT	coagulation factor
10	13	5.2	593	2 S45281	coagulation factor
11	13	5.2	603	2 S28941	coagulation factor
12	13	5.2	615	1 KFHU12	polypotein - Afri
13	13	5.2	1524	2 T30337	complement factor
14	12	4.8	191	2 S54115	trypsin-like prote
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17	12	4.8	264	2 S32794	trypsin (EC 3.4.21
18	12	4.8	267	2 S40006	serine proteinase
19	12	4.8	271	2 S41308	trypsin (EC 3.4.21
20	12	4.8	274	2 S35339	trypsin (EC 3.4.21
21	12	4.8	275	2 S40007	trypsin (EC 3.4.21
22	12	4.8	275	2 S40005	trypsin (EC 3.4.21
23	12	4.8	287	2 S35340	probable serine pr
24	12	4.8	285	2 T35195	chymotrypsin-like
25	11	4.4	126	2 A23473	probable serine pr
26	11	4.4	225	2 S45356	serine proteinase
27	11	4.4	237	2 S55378	trypsin (EC 3.4.2
28	11	4.4	237	2 S68702	neuropsin - mouse
29	11	4.4	260	2 S56559	

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32	11	4.4	270	2 S56160	mast cell tryptase
33	11	4.4	273	2 A47246	tryptase (EC 3.4.2
34	11	4.4	274	2 JC4171	tryptase (EC 3.4.2
35	11	4.4	275	2 A35863	tryptase (EC 3.4.2
36	11	4.4	275	2 B35863	tryptase (EC 3.4.2
37	11	4.4	275	2 A32410	tryptase (EC 3.4.2
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39	11	4.4	276	2 A38654	coagulation factor
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41	11	4.4	343	1 A57014	coagulation factor
42	11	4.4	400	1 A48050	u-plasminogen acti
43	11	4.4	431	1 UKHUV	u-plasminogen acti
44	11	4.4	433	1 UKHAY	u-plasminogen acti
45	11	4.4	433	1 JN0560	u-plasminogen acti

ALIGNMENTS

RESULT 1

DBHU

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N;Alternate names: adipain; C3 convertase activator
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 31-Dec-1992 #text_change 08-Dec-2000
C;Accession: A40197; A00936; A60571; S66645
R;White, R.T.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.
J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipain is identical to complement factor D and is expressed at high lev
A;Reference number: A40197; MUID:92250520; PMID:1374388
A;Accession: A40197
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A;Residues: 1-246 <WHI>
A;Cross-references: GB:M84526
R;Niemann, M.A.; Bhowm, A.S.; Bennett, J.C.; Volanakis, J.E.
Biochemistry 23, 2482-2486, 1984
A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
A;Accession: A00936
A;Molecule type: protein
A;Residues: 19-44 'G', 46-51 'Q', 53-75 'TH', 78 'P', 80-83 'XXXITIE', 90-172, 86-91, 185-235,
A;Note: a few residues were assigned from the previously published sequence of Reid et
R;Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Y
Mol. Immunol. 27, 637-644, 1990
A;Title: Molecular and functional identification and purification of complement compo
A;Reference number: A60571; MUID:90370044; PMID:2395435
A;Accession: A60571
A;Molecule type: protein
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R;Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A;Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complemen
A;Reference number: S66645; MUID:96013156; PMID:7556615
A;Accession: S66645
A;Status: preliminary
A;Molecule type: protein
A;Residues: 19-44 'C', 46-48 <BAL>
C;Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, acti
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A;Gene: GDB:DF
A;Cross-references: GDB:I32645; OMIM:134350
A;Map position: Xpter-Xqter
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
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P;19-241/Domain: trypsin homology <TRY>
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P;59, 105, 201/Active site: His, Asp, Ser #status predicted

Query Match

5.2%; Score 13; DB 1; Length 246;

Best Local Similarity 100.0%; Pred. No. 2.9e-05; Mismatches 0; Indels 0; Gaps 0;

Query 198 GDSGGPLVCGGVL 210
 |||||
 Db 199 GDSGGPLVCGGVL 211

RESULT 2

JS0600

t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat

N:Alternate names: tissue plasminogen activator

C:Species: Desmodus rotundus (common vampire bat)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: JS0600

R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don

Gene 105, 229-237, 1991

A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des

A:Reference number: JS0597; MUID:92039036; PMID:1937019

A:Accession: JS0600

A:Molecule type: mRNA

A:Residues: 1-394 <KRA>

A:Cross-references: GB:M63990; NID:G166078; PIDN:AAA31595.1; PID:G166079

A>Note: the authors translated the codon ATC for residue 75 as Thr

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-36/Domain: propeptide #status predicted <PRO>

F:37-394/Product: plasminogen activator gamma #status predicted <PLA>

F:45-126/Domain: kringle homology <KRG>

F:143-388/Domain: trypsin homology <TRY>

F:45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:

F:142-143/Cleavage site: His-Ser (plasmin) #status predicted

F:189,238,345/Active site: His, Asp, Ser #status predicted

F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 5.2%; Score 13; DB 2; Length 394;

Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;

Query 194 DACQSDSGGPLVC 206
 |||||
 Db 339 DACQSDSGGPLVC 351

RESULT 3

JS0599

t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat

N:Alternate names: tissue plasminogen activator

C:Species: Desmodus rotundus (common vampire bat)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: JS0599

R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don

Gene 105, 229-237, 1991

A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des

A:Reference number: JS0597; MUID:92039036; PMID:1937019

A:Accession: JS0599

A:Molecule type: mRNA

A:Residues: 1-431 <KRA>

A:Cross-references: GB:M63989; NID:G166076; PIDN:AAA31594.1; PID:G166077

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-36/Domain: propeptide #status predicted <PRO>

F:37-431/Product: plasminogen activator beta #status predicted <PLA>

F:41-74/Domain: EGF homology <EGF>

F:82-163/Domain: kringle homology <KRG>

F:180-425/Domain: trypsin homology <TRY>

F:41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bon

F:139,352/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:179-180/Cleavage site: His-Ser (plasmin) #status predicted

F:226,275,382/Active site: His, Asp, Ser #status predicted

F:345-361,378-406/Disulfide bonds: #status predicted

Query Match 5.2%; Score 13; DB 2; Length 431;

Best Local Similarity 100.0%; Pred. No. 4.7e-05; Mismatches 0; Indels 0; Gaps 0;

Query 194 DACQSDSGGPLVC 206
 |||||
 Db 376 DACQSDSGGPLVC 388

RESULT 4

JS04369

t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)

C:Species: Megaderma lyra

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A34369

R:Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jaco

J. Biol. Chem. 264, 17947-17952, 1989

A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmi

A:Reference number: A34369; MUID:90036867; PMID:2509450

A:Accession: A34369

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-477 <GAR>

A:Cross-references: GB:J05082; NID:G166080; PIDN:AAA31596.1; PID:G166081

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat h

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-36/Domain: propeptide #status predicted <PRO>

F:37-477/Product: plasminogen activator #status predicted <PLA>

F:42-79/Domain: fibronectin type I repeat homology <1FA>

F:87-120/Domain: EGF homology <EGF>

F:128-209/Domain: kringle homology <KRG>

F:226-471/Domain: trypsin homology <TRY>

F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-

P:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 5.1e-05; Mismatches 0; Indels 0; Gaps 0;

Query 194 DACQSDSGGPLVC 206
 |||||
 Db 422 DACQSDSGGPLVC 434

RESULT 5

JS0597

t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat

N:Alternate names: tissue plasminogen activator

C:Species: Desmodus rotundus (common vampire bat)

C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

C:Accession: JS0597

R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dc

Gene 105, 229-237, 1991

A:Title: The plasminogen activator family from the salivary gland of the vampire bat De

A:Reference number: JS0597; MUID:92039036; PMID:1937019

A:Accession: JS0597

A:Molecule type: mRNA

A:Residues: 1-477 <KRA>

A:Cross-references: GB:M63987; NID:G166070; PIDN:AAA31591.1; PID:G166071

C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat h

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-36/Domain: propeptide #status predicted <PRO>

F:37-477/Product: plasminogen activator alpha-1 #status predicted <PLA>

F:42-79/Domain: fibronectin type I repeat homology <1FA>

F:87-120/Domain: EGF homology <EGF>

F:128-209/Domain: kringle homology <KRG>

F:226-471/Domain: trypsin homology <TRY>

F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-

P:153,398/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:225-226/Cleavage site: His-Ser (plasmin) #status predicted

F;272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 5,1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206

|||||

Db 422 DACQDSGGPLVC 434

RESULT 6

JS0598

t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat

N;Alternate names: tissue plasminogen activator

C;Species: Desmodus rotundus (common vampire bat)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

A;Accession: JS0598

R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alegon, A.; Don

Gene 105, 229-237, 1991

A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des

A;Reference number: JS0597; MUID:92039036; PMID:1937019

A;Accession: JS0598

A;Molecule type: mRNA

A;Residues: 1-477 <KRA>

A;Cross-references: GB:M63988; NID:gi166074; PIDN:AAA1593.1; PID:gi166075

C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-36/Domain: propeptide #status predicted <PRO>

F;37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>

F;42-79/Domain: fibronectin type I repeat homology <1PA>

F;87-120/Domain: EGF homology <EGF>

F;128-209/Domain: kringle homology <KRG>

F;226-471/Domain: trypsin homology <TRY>

F;42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4

F;185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;225-226/Cleavage site: His-Ser (plasmin) #status predicted

F;272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 2; Length 477;

Best Local Similarity 100.0%; Pred. No. 5,1e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206

|||||

Db 422 DACQDSGGPLVC 434

RESULT 7

A35029

t-plasminogen activator (EC 3.4.21.68) precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

A;Accession: A35029; A31597

R;Feng, P.; Ohlsson, M.; Ny, T.

J. Biol. Chem. 265, 2022-2027, 1990

A;Title: The structure of the TARA-less rat tissue-type plasminogen activator gene. Sped

A;Reference number: A35029; MUID:90130448; PMID:2105315

A;Accession: A35029

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-559 <PEN>

A;Cross-references: GB:M31197; NID:g207429; PIDN:AAA42261.1; PID:g207431; GB:J05226

R;Ny, T.; Leonardsson, G.; Hsueh, A.J.W.

DNA 7, 671-677, 1988

A;Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activat

A;Reference number: A31597; MUID:89170114; PMID:3148445

A;Accession: A31597

A;Molecule type: mRNA

A;Residues: 1-379, 'K', 381-559 <NTY>

A;Cross-references: GB:M23697; NID:g530159; PIDN:AAA41812.1; PID:g530160

C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-29/Domain: propeptide #status predicted <PRO>

F;30-559/Product: t-plasminogen activator #status predicted <MAT>

F;38-75/Domain: fibronectin type I repeat homology <1P1>

F;83-116/Domain: EGF homology <EGF>

F;124-205/Domain: kringle homology <KR1>

F;213-294/Domain: kringle homology <KR2>

F;309-559/Product: t-plasminogen activator chain B #status predicted <BCH>

F;309-553/Domain: trypsin homology <TRY>

F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297--

F;149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted

F;355,404,510/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 1; Length 559;

Best Local Similarity 100.0%; Pred. No. 5,9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206

|||||

Db 504 DACQDSGGPLVC 516

RESULT 8

A29941

t-plasminogen activator (EC 3.4.21.68) precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: A29941; S48205; S48207; S48206

R;Rickles, R.J.; Darrow, A.L.; Strickland, S.

J. Biol. Chem. 263, 1563-1569, 1988

A;Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator m

A;Reference number: A29941; MUID:88087303; PMID:2826484

A;Accession: A29941

A;Molecule type: mRNA

A;Residues: 1-559 <KIC>

A;Cross-references: GB:J03520; NID:g202109; PIDN:AAA0470.1; PID:g202110

R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.

Eur. J. Biochem. 224, 863-871, 1994

A;Title: Characterization of the murine plasma fibrinolytic system.

A;Reference number: S48202; MUID:95010076; PMID:7523120

A;Accession: S48205

A;Molecule type: protein

A;Residues: 33-37, 'X', 39-40 <LIJ>

A;Accession: S48207

A;Molecule type: protein

A;Residues: 309-316 <LIZ>

A;Accession: S48206

A;Molecule type: protein

A;Residues: 33-37, 'X', 39-40 <LIW>

C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hoi

C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase

F;1-17/Domain: signal sequence #status predicted <SIG>

F;18-29/Domain: propeptide #status predicted <PRO>

F;30-559/Product: t-plasminogen activator #status predicted <MAT>

F;38-75/Domain: fibronectin type I repeat homology <1P1>

F;83-116/Domain: EGF homology <EGF>

F;124-205/Domain: kringle homology <KR1>

F;213-294/Domain: kringle homology <KR2>

F;309-559/Product: t-plasminogen activator chain B #status predicted <BCH>

F;309-553/Domain: trypsin homology <TRY>

F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297--

F;149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted

F;355,404,510/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 1; Length 559;

Best Local Similarity 100.0%; Pred. No. 5,9e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 194 DACQDSGGPLVC 206
 |||||
 Db 504 DACQDSGGPLVC 516

RESULT 9

UKRUT

t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human
 N;Alternate names: t-PA; tissue plasminogen activator

C;Species: Homo sapiens (man)

C;Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000

C;Accession: A94004; A23529; J70562; A93293; S02125; A91343; A93951; A91322; A54645; I60

R;NY, I.; Elgin, F.; Lund, B.

Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984

A;Title: The structure of the human tissue-type plasminogen activator gene: correlation

A;Reference number: A94004; MUID:84298137; PMID:6089198

A;Accession: A94004

A;Molecule type: DNA

A;Residues: 1-562 <N>

A;Cross-references: GB:L00141

A;Note: the codon given for residue 93 (ACC) is inconsistent with the authors' translation

R;Friedman Degen, S.J.; Rajput, B.; Reich, E.

J. Biol. Chem. 261, 6972-6985, 1986

A;Title: The human tissue plasminogen activator gene.

A;Reference number: A23529; MUID:86196143; PMID:3009482

A;Accession: A23529

A;Molecule type: DNA

A;Residues: 1-562 <DRG>

A;Cross-references: GB:K03021; NID:g339817; PIDN:AAA98809.1; PID:g339818

R;Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuoka, S.; Higashio, K.

Agric. Biol. Chem. 55, 1225-1232, 1991

A;Title: Purification and characterization of tissue plasminogen activator secreted by H

A;Reference number: J70562; MUID:91291340; PMID:1368681

A;Accession: J70562

A;Molecule type: mRNA

A;Residues: 31-562 <ITA>

A;Cross-references: DBJ:D01096; NID:g220128; PIDN:BA00881.1; PID:g441174

A;Experimental source: embryonic lung fibroblast IMR-90 cells

A;Note: part of this sequence, including the amino end of the mature protein, was confir

R;Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett

Nature 301, 214-221, 1983

A;Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche

A;Reference number: A93293; MUID:83115262; PMID:6337343

A;Accession: A93293

A;Molecule type: mRNA

A;Residues: 1-562 <PEN>

A;Cross-references: GB:L00141

A;Experimental source: melanoma cells

R;Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.

Nucleic Acids Res. 16, 5695, 1988

A;Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe

A;Reference number: S02125; MUID:88262579; PMID:3133640

A;Accession: S02125

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-562 <SAS>

A;Cross-references: EMBL:X07393; NID:g37243; PIDN:CAA30302.1; PID:g37244

A;Experimental source: fetal lung cells

R;Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma

FEBS Lett. 189, 145-149, 1985

A;Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen

A;Reference number: A91343; MUID:85285620; PMID:3896853

A;Accession: A91343

A;Molecule type: mRNA

A;Residues: 1-38, 'G', 'E', 435-562 <KAG>

A;Experimental source: Detroit 562 cells; ATCC 138

R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.

Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983

A;Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ

A;Reference number: A93951; MUID:83169656; PMID:6572897

A;Accession: A93951

A;Molecule type: mRNA

A;Residues: 251-358 <EDL>

A;Experimental source: melanoma cells
 R;Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
 Biochemistry 23, 3701-3707, 1984
 A;Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived a
 differences.
 A;Reference number: A90488; MUID:85000468; PMID:6433976
 A;Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and
 R;Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
 FEBS Lett. 168, 29-32, 1984
 A;Title: Differences between uterine and melanoma forms of tissue plasminogen activator
 A;Reference number: A91322; MUID:84158956; PMID:6538514
 A;Accession: A91322
 A;Molecule type: protein
 A;Residues: 33-45;311-320 <POH>
 A;Experimental source: uterus
 A;Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
 R;van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
 J. Biol. Chem. 261, 14214-14218, 1986
 A;Reference number: A37567; MUID:87033611; PMID:3021732
 A;Contents: annotation; fibrin binding site
 R;Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enga
 EMBO J. 5, 3525-3530, 1986
 A;Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen a
 A;Reference number: A37568; MUID:87161761; PMID:3030730
 A;Contents: annotation; fibrin binding site
 R;Dodd, I.; Nunn, B.; Robinson, J.H.
 Thromb. Haemost. 59, 523-528, 1988
 A;Title: Isolation, identification and pharmacokinetic properties of human tissue-type
 A;Reference number: A60902; MUID:89044681; PMID:3142086
 A;Contents: annotation; novel forms of expressed recombinant t-PA
 R;Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Emtage, J.S.; Opdenakker, G.;
 Mol. Biol. Med. 3, 279-292, 1986
 A;Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its exp
 A;Reference number: A54645; MUID:86284200; PMID:3090401
 A;Accession: A54645
 A;Molecule type: mRNA
 A;Residues: 1-562 <HAR>
 A;Cross-references: GB:M5518; NID:g190031; PIDN:AAA60111.1; PID:g190032
 A;Note: parts of this sequence were confirmed by peptide sequencing
 R;Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
 DNA 6, 461-472, 1987
 A;Title: Expression of human uterine tissue-type plasminogen activator in mouse cells u
 A;Reference number: I60110; MUID:88054470; PMID:2824147
 A;Accession: I60110
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-562 <RES>
 A;Cross-references: GB:M18182; NID:g340176; PIDN:AAA36800.1; PID:g340177
 R;Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
 J. Biol. Chem. 260, 11223-11230, 1985
 A;Title: Isolation and characterization of the human tissue-type plasminogen activator
 A;Reference number: I55232; MUID:85289338; PMID:3161893
 A;Accession: I55232
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-36 <RES>
 A;Cross-references: GB:M1890; NID:g339837; PIDN:AAA61213.1; PID:g339839
 C;Comment: Cleavage by plasmin or trypsin produces two chains held together by a single
 C;Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. I
 C;Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
 C;Genetics:
 A;Gene: GDB:PLAT
 A;Cross-references: GDB:I19496; OMIM:173370
 A;Map position: 9p12-9p12
 A;Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 51
 C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat ho
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-32/Domain: propeptide #status predicted <PRO>
 F;33-562/Product: t-plasminogen activator #status experimental <MAT>
 F;33-310/Product: t-plasminogen activator chain A #status experimental <ACH>
 F;41-78/Domain: fibronectin type I repeat homology <IFI>
 F;86-119/Domain: EGF homology <EGF>

A;Reference number: S28941; MUID:93003367; PMID:1390917
A;Accession: S28941
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-603 <SEM>
A;Cross-references: EMBL:X68615; NID:949578; PIDN:CAA48600.1; PID:949579
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology
C;Keywords: hydrolase; serine proteinase
F;46-87/Domain: fibronectin type II repeat homology <1P2>
F;134-169/Domain: fibronectin type I repeat homology <Fb1>
F;177-208/Domain: EGF homology <EGF>
F;216-294/Domain: kringle homology <KRG>
F;359-597/Domain: trypsin homology <TRY>

Query Match 5.2%; Score 13; DB 2; Length 603;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDGGGLPVC 206
|||||
Db 545 DACQDGGGLPVC 557

RESULT 12
KFHUI2
coagulation factor XIIa (SC 3.4.21.38) precursor [validated] - human
N;Alternate names: Hageman factor (activated)
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence revision 30-Jun-1991 #text change 08-Dec-2000
C;Accession: A29411; A26814; A00930; A25191; A22248; A21037
J;Cool, D.E.; MacGillivray, R.T.A.
J. Biol. Chem. 262, 13662-13673, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon g
A;Reference number: A29411; MUID:88007593; PMID:2888762
A;Accession: A29411
A;Molecule type: DNA
A;Residues: 1-615 <COO>
A;Cross-references: GB:M17466; GB:J02807; NID:gl80355; PIDN:AAB59490.1; PID:gl80357
R;Trippodi, M.; Citarella, F.; Guida, S.; Galeffi, P.; Pantoni, A.; Cortese, R.
Nucleic Acids Res. 14, 3146, 1986
A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).
A;Reference number: A26814; MUID:86176794; PMID:3754331
A;Accession: A26814
A;Molecule type: mRNA
A;Residues: 4-615 <TRI>
A;Cross-references: GB:M31315; NID:gl82291; PIDN:AAA70225.1; PID:gl82292
P;Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R.
J. Biol. Chem. 260, 13668-13676, 1985
A;Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the
A;Reference number: A00930; MUID:86033830; PMID:3877053
A;Accession: A00930
A;Molecule type: mRNA
A;Residues: 14-332, 'S', 334-615 <CO2>
A;Cross-references: GB:M11723; NID:gl80358; PIDN:AAAS1986.1; PID:gl80359
R;Que, B.G.; Davie, E.W.
Biochemistry 25, 1525-1528, 1986
A;Title: Characterization of a cDNA coding for human factor XII (Hageman factor).
A;Reference number: A25191; MUID:86216049; PMID:3011063
A;Accession: A25191
A;Molecule type: mRNA
A;Residues: 146-378, 'G', 380-615 <QUB>
A;Cross-references: GB:M33147; NID:gl80360; PIDN:AAA70224.1; PID:gl80361
R;McMullen, B.A.; Fujikawa, K.
J. Biol. Chem. 260, 5328-5341, 1985
A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated H
A;Reference number: A22248; MUID:85182674; PMID:3886654
A;Accession: A22248
A;Molecule type: protein
A;Residues: 20-379 <MCM>
R;Fujikawa, K.; McMullen, B.A.
J. Biol. Chem. 258, 10924-10933, 1983
A;Title: Amino acid sequence of human beta-factor XIIa.
A;Reference number: A21037; MUID:83291041; PMID:6604055

A;Accession: A21037
A;Molecule type: protein
A;Residues: 354-362;373-615 <FUU>
R;Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucose is present in the first epidermal growth factor domain of factor X.
A;Reference number: A44606; MUID:92184750; PMID:1544894
A;Contents: annotation; carbohydrate binding site
C;Genetics:
A;Gene: GDB:F12
A;Cross-references: GDB:119892; OMIM:234000
A;Map position: 5q34-5qter
A;Introns: 19/3; 39/1; 72/1; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 463/1; 511/1
C;Complex: factor XII, prekallikrein, and HMW kininogen form a complex bound to anionic site.
C;Function:
A;Description: factor XIIa catalyzes the proteolytic activation of plasminogen, plasma prekallikrein.
A;Pathway: blood coagulation; fibrinolysis
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology; F1-19/Domains: signal sequence #status predicted <SIG>
F;120-372,373-615/Product: coagulation factor XIIa, alpha form #status experimental <A12>
F;47-88/Domains: fibronectin type II repeat homology <FB2>
F;98-130/Domains: EGF homology <EG1>
F;135-170/Domains: fibronectin type I repeat homology <IF1>
F;178-209/Domains: EGF homology <EG2>
F;217-295/Domains: kringle homology <KRG>
F;298-356/Region: proline-rich
F;354-362,373-615/Product: coagulation factor XIIa, beta form #status experimental <B12>
F;373-609/Domains: trypsin homology <TRY>
F;98-110,104-119,121-130,135-163,161-170,178-189,183-198,200-209,217-295,238-277,266-290
F;109/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;249,433/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F;308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;412,461,563/Active site: His, Asp, Ser #status predicted

Query Match 5.2%; Score 13; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSDGGPLVC 206
Db 557 DACQDSDGGPLVC 569

RESULT 13
T30337
polyprotein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
C;Accession: T30337
R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from Xenopus oocytes.
A;Reference number: 220829
A;Accession: T30337
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1524 <YAN>
A;Cross-references: EMBL:U01290; NID:g2981640; PID:g2981641; PIDN:AAC24717.1
C;Superfamily: tryosin related polyprotein; trypsin homology

Query Match 5.2%; Score 13; DB 2; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSDGGPLVC 206
Db 762 DACQDSDGGPLVC 774

RESULT 14

S54115
complement factor D (BC 3.4.21.46) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 19-May-2000
C;Accession: S54115
R;Nicolas, N.
submitted to the EMBL Data Library, April 1995
A;Reference number: S54115
A;Accession: S54115
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-191 <NIC>
A;Cross-references: EMBL:Z49058; NID:g773264; PIDN:CAA88844.1; PID:g773265
C;Superfamily: trypsin; trypsin homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-181/Domains: trypsin homology (fragment) <TRY>

Query Match 4.8%; Score 12; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 GDSGGLVCGGV 209
Db 139 GDSGGLVCGGV 150

RESULT 15
S65465
trypsin-like proteinase (EC 3.4.21.-) precursor - flesh fly (Sarcophaga bullata)
C;Species: Sarcophaga bullata
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S65465; S65403
R;Borovsky, D.; Janssen, I.; Vanden Broeck, J.; Huybrechts, R.; Verhaert, P.; de Bondt, R.; J. Biochem. 237, 279-287, 1996
A;Title: Molecular sequencing and modeling of Neobellieria bullata trypsin. Evidence for a new trypsin-like proteinase.
A;Reference number: S65403; MUID:96203936; PMID:8620885
A;Accession: S65465
A;Molecule type: mRNA
A;Residues: 1-254 <BOR>
A;Cross-references: EMBL:X94691; NID:g1177315; PIDN:CAA64354.1; PID:g1177316
A;Accession: S65403
A;Molecule type: protein
A;Residues: 27-36 <BOR>
A;Note: 27-Leu, 35-Leu were also found
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;1-16/Domains: signal sequence #status predicted <SIG>
F;17-26/Domains: propeptide #status predicted <PRO>
F;27-254/Product: trypsin #status experimental <MAT>
F;27-247/Domains: trypsin homology <TRY>
F;53-69,154-158,195-238,204-228/Diulfide bonds: #status predicted
F;68,113,208/Active site: His, Asp, Ser #status predicted

Query Match 4.8%; Score 12; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSDGGPLV 205
Db 202 DACQDSDGGPLV 213

Search completed: June 16, 2004, 15:15:32
Job time : 21 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 16, 2004, 15:07:31 ; Search time 17 Seconds
(without alignments)
759.612 Million cell updates/sec

Title: US-10-006-116A-194

Perfect score: 248

Sequence: 1 MGLSIFLLCLVGLSQATP.....GVVTVICKYVDWIRIMRN 248

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	248	100.0	248	1	KLKC_HUMAN	O9ukr0 homo sapien
2	13	5.2	253	1	CPAD_HUMAN	P00746 homo sapien
3	13	5.2	394	1	URTB_DESRO	P49150 desmodus ro
4	13	5.2	431	1	URTB_DESRO	P98121 desmodus ro
5	13	5.2	455	1	TMS5_MOUSE	O9er04 mus musculus
6	13	5.2	457	1	TMS5_HUMAN	O9h3a3 homo sapien
7	13	5.2	477	1	URTB_DESRO	P98119 desmodus ro
8	13	5.2	477	1	URTB_DESRO	P15638 desmodus ro
9	13	5.2	559	1	TPA_MOUSE	F11214 mus musculus
10	13	5.2	559	1	TPA_RAT	F19637 rattus norv
11	13	5.2	562	1	TPA_HUMAN	P00750 homo sapien
12	13	5.2	566	1	TPA_BOVIN	O28198 bos taurus
13	13	5.2	593	1	PA12_BOVIN	P98140 bos taurus
14	13	5.2	603	1	PA12_CAVPO	O04962 cavia porce
15	13	5.2	615	1	PA12_HUMAN	P00748 homo sapien
16	13	5.2	653	1	HGPA_MOUSE	O9r098 mus musculus
17	13	5.2	811	1	TMS6_HUMAN	O81u80 homo sapien
18	13	5.2	811	1	TMS6_MOUSE	O9dbi0 mus musculus
19	12	4.8	244	1	KLK6_HUMAN	O92876 homo sapien
20	12	4.8	253	1	TRYB_DROER	P54625 drosophila
21	12	4.8	253	1	TRYD_DROER	P54626 drosophila
22	12	4.8	253	1	TRYD_DROME	P42276 drosophila
23	12	4.8	253	1	TRYD_DROME	P42277 drosophila
24	12	4.8	254	1	TRYP_SARBU	P51588 sarcophaga
25	12	4.8	256	1	HYPB_HYPLI	P35588 hypodema 1
26	12	4.8	256	1	TRYA_DROER	P54624 drosophila
27	12	4.8	256	1	TRYA_DROME	P04814 drosophila
28	12	4.8	256	1	TRYE_DROER	P54627 drosophila
29	12	4.8	256	1	TRYE_DROME	P35005 drosophila
30	12	4.8	258	1	TRYD_DROER	P54629 drosophila
31	12	4.8	259	1	CFAD_PIG	P51779 sus scrofa
32	12	4.8	262	1	TRYD_DROME	P42279 drosophila
33	12	4.8	264	1	VDP_BOMMO	Q007943 bombyx mori

RESULT 1

ID	KLKC_HUMAN	STANDARD;	PRT;	248 AA.
AC	O9UKR0; O9UKR1;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DB	Kallikrein 12 precursor (EC 3.4.21.-) (Kallikrein-like protein 5)			
DE	(KLK-L5).			
GN	KLK12 OR KLK15.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Rutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20118156; PubMed=10652563;			
RA	Yousef G.M., Luo L.-Y., Diamandis E.P.;			
RT	"Identification of novel human kallikrein-like genes on chromosome			
RT	19q13.3-q13.4.";			
RL	Anticancer Res. 19:2843-2852(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Yousef G.M., Magklara A., Scorilas A., Diamandis E.P.;			
RT	"Cloning of new alternatively spliced forms of the kallikrein-like			
RT	gene 5 (KLK-L5).";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=20510030; PubMed=11054574;			
RA	Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,			
RA	Moss P., Paepfer B., Wang K.;			
RT	"Sequencing and expression analysis of the serine protease gene			
RT	cluster located in chromosome 19q13 region.";			
RL	Gene 257:119-130(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RA	Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,			
RA	Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,			
RA	Phan H., Velasco N., Do L., Regala M., Terry A., Brower A., Gaines J.,			
RA	Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,			
RA	Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,			
RA	Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,			
RA	Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,			
RA	Olsen A.S., Carrano A.V.;			
RT	"Sequence analysis of chromosome 19q13.4.";			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
CC	-I- SUBCELLULAR LOCATION: Secreted (Probable).			
CC	-I- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	isoId=O9UKR0-1; Sequence=Displayed;			
CC	Name=2;			
CC	isoId=O9UKR0-2; Sequence=VSP_005403;			
CC	-I- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.			

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DR EMBL; AF135025; AAD26426.2; -
DR EMBL; AF135025; AAF06065.1; -
DR EMBL; AF243527; AAG33365.1; -
DR EMBL; AC011473; AAG23258.1; -
DR HSP; P00763; IDPO.
DR MEROPS; S01.020; -
DR Genew; HGNC:6360; KLIK12.
DR MIM; 605539; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:004252; P:serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Signal;
KW Alternative splicing.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 248 KALLIKREIN 12.
FT ACT_SITE 62 62 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 200 200 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 28 161 BY SIMILARITY.
FT DISULFID 47 63 BY SIMILARITY.
FT DISULFID 133 235 BY SIMILARITY.
FT DISULFID 140 206 BY SIMILARITY.
FT DISULFID 172 186 BY SIMILARITY.
FT DISULFID 196 222 BY SIMILARITY.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPIC 163 163 KYDWRIMRMNN -> NSTVLGTSNPNFSCQPF (in isoform 2).
FT FTID-VSP 005403.
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Query Match 100.0%; Score 248; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 7.9e-255; Mismatches 0; Indels 0; Gaps 0;
Matches 248; Conservative 0;

QY 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNQSPQWQVGLFECTSLRCGGVLIDHRWLTA 60
Db 1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNQSPQWQVGLFECTSLRCGGVLIDHRWLTA 60

QY 61 AHCSGSRYVRVLGHSLSQLDWTQIRHSGFVSHTPGVYLGASTSHEHDLRLRLPVRV 120
Db 61 AHCSGSRYVRVLGHSLSQLDWTQIRHSGFVSHTPGVYLGASTSHEHDLRLRLPVRV 120

QY 121 TSSVQPLPLPNDCACTAGTECHVSGHGTTHNPNRPDLLOCLNLSIVSHATCHGVYVGR 180
Db 121 TSSVQPLPLPNDCACTAGTECHVSGHGTTHNPNRPDLLOCLNLSIVSHATCHGVYVGR 180

QY 181 TSNMYCAGVPQDQACQDGSGLPVCVGLQGLVSGVSGVPGCGQDGI PGVYTYICKYVDW 240
Db 181 TSNMYCAGVPQDQACQDGSGLPVCVGLQGLVSGVSGVPGCGQDGI PGVYTYICKYVDW 240

QY 241 IRMIMRNN 248
Db 241 IRMIMRNN 248

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RESULT 2
ID CPAD_HUMAN STANDARD; PRT; 253 AA.
AC P00746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Complement factor D precursor (EC 3.4.21.46) (C3 convertase activator)
DE (Properdin factor D) (Adipsin).
GN DF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE OF 8-253 FROM N.A.
RX MEDLINE=92250520; PubMed=1374388;
RA White R.T., Damm D., Hancock N., Rosen B.S., Lowell B.B., Usher P.,
RA Plier J.S., Spiegelman B.M.;
RT "Human adipsin is identical to complement factor D and is expressed
RT at high levels in adipose tissue.";
RL J. Biol. Chem. 267:9210-9213(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Plier J.S., Spiegelman B.M., Rosen B.M.;
RL Patent number W09006365, 14-JUN-1990.
RN [3]
RP SEQUENCE OF 26-252.
RX MEDLINE=85000441; PubMed=6383466;
RA Niemann M.A., Bhowan A.S., Bennett J.C., Volanakis J.E.;
RT "Amino acid sequence of human D of the alternative complement
RT pathway.";
RL Biochemistry 23:2482-2486(1984).
RN [4]
RP PARTIAL SEQUENCE OF 26-252.
RX MEDLINE=84108950; PubMed=6363133;
RA Johnson D.M.A., Gagnon J., Reid K.B.M.;
RT "Amino acid sequence of human factor D of the complement system.
RT Similarity in sequence between factor D and proteases of non-plasma
RT origin.";
RL FEBS Lett. 166:347-351(1984).
RN [5]
RP PARTIAL SEQUENCE OF 26-61 AND 194-220.
RX MEDLINE=84256515; PubMed=6821372;
RA Johnson D.M.A., Gagnon J., Reid K.B.M.;
RT "Factor D of the alternative pathway of human complement.
RT Purification, alignment and N-terminal amino acid sequences of the
RT major cyanogen bromide fragments, and localization of the serine
RT residue at the active site.";
RL Biochem. J. 187:863-874(1980).
RN [6]
RP PARTIAL SEQUENCE OF 26-82.
RX MEDLINE=80145719; PubMed=6987665;
RA Volanakis J.E., Bhowan A.S., Bennett J.C., Mole J.E.;
RT "Partial amino acid sequence of human factor D:homology with serine
RT proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:1116-1119(1980).
RN [7]
RP PARTIAL SEQUENCE OF 26-78.
RX MEDLINE=81054886; PubMed=6776531;
RA Davis A.E. III;
RT "Active site amino acid sequence of human factor D.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:4938-4942(1980).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=94118317; PubMed=8289289;
RA Narayana S.V.L., Carson M., El-Kabbani O., Kilpatrick J.M., Moore D.,
RA Chen X., Bugg C.E., Volanakis J.E., Deluca L.J.;
RT "Structure of human factor D. A complement system protein at 2.0-A
RT resolution.";
RL J. Mol. Biol. 235:695-708(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

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RX MEDLINE=96025834; PubMed=7592653;
RA Kim S., Narayana S.V., Volanakis J.E.;
RT "Crystal structure of a complement factor D mutant expressing
enhanced catalytic activity.";
RL J. Biol. Chem. 270:24399-24405(1995).
CC -|- FUNCTION: Factor D cleaves factor B when the latter is complexed
with factor C3b, activating the C3bb complex, which then becomes
the C3 convertase of the alternate pathway. Its function is
homologous to that of C1s in the classical pathway.
CC -|- CATALYTIC ACTIVITY: Cleaves component factor B (Arg-|-Lys) when in
complex with C3b or with cobra venom factor (CVF).
CC -|- SIMILARITY: Belongs to peptidase family S1.
CC -|- CAUTION: In addition to the conflicts shown in the feature table,
Ref.3 sequence had a peptide in the wrong order and another one
missing.
CC
CC
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CC -----
DR EMBL; M84526; AAA35527.1; ALT_INIT.
DR PIR; A40197; DRHU.
DR PDB; 1DPP; 25-FEB-98.
DR PDB; 1DST; 11-JUL-96.
DR PDB; 1DSU; 17-AUG-96.
DR PDB; 1BIO; 22-JUN-99.
DR PDB; 1DIC; 22-JUL-99.
DR PDB; 1FDP; 03-DEC-99.
DR PDB; 1HFD; 22-JUN-99.
DR MEROPS; S01.191; -.
DR Genew; HGNC:2771; DF.
DR MIM; 134350; -.
DR GO; GO:0003817; P:complement factor D activity; TAS.
DR GO; GO:0008236; P:serine-type peptidase activity; TAS.
DR GO; GO:0006956; P:complement activation; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KMW Complement alternate pathway; Plasma; Hydrolase; Serine protease;
Zymogen; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 20
FT PROPEP 21 25 POTENTIAL.
FT CHAIN 26 253 COMPLEMENT PEPTIDE (POTENTIAL).
FT ACT_SITE 66 66 COMPLEMENT FACTOR D.
FT ACT_SITE 112 112 CHARGE RELAY SYSTEM.
FT ACT_SITE 208 208 CHARGE RELAY SYSTEM.
FT DISULFID 51 67 CHARGE RELAY SYSTEM.
FT DISULFID 148 214
FT DISULFID 179 195
FT DISULFID 204 229
FT CONFLICT 26 26
FT CONFLICT 35 35
FT CONFLICT 40 40
FT CONFLICT 49 49
FT CONFLICT 52 52
FT CONFLICT 59 59
FT CONFLICT 63 63
FT CONFLICT 73 73
FT CONFLICT 83 86
FT CONFLICT 83 84
FT CONFLICT 94 95
FT CONFLICT 96 96
I -> M (IN REF. 1).
H -> F (IN REF. 6).
M -> V (IN REF. 6).
H -> E (IN REF. 4 AND 5).
G -> A (IN REF. 1 AND 2).
Q -> R (IN REF. 1 AND 2).
S -> T (IN REF. 4).
D -> G (IN REF. 4).
HSLs -> THLP (IN REF. 3).
HS -> ST (IN REF. 4).
MISSING (IN REF. 4).
D -> E (IN REF. 4).

Q -> G (IN REF. 4).
TCNRRTHDGAITE -> KCRLYDVL (IN REF. 4).
S -> T (IN REF. 3).
S -> H (IN REF. 3).
MISSING (IN REF. 4).
136 136
191 178
243 243
250 243
250 250
250 250
27 27
28 28
31 31
35 35
39 39
45 45
47 47
57 48
59 58
63 60
65 65
70 66
80 76
84 84
91 90
102 93
105 104
113 112
120 116
127 127
129 128
130 130
135 135
145 144
152 147
159 158
165 165
173 167
182 176
184 183
192 191
196 193
202 202
204 204
206 205
209 208
214 211
216 215
222 217
226 226
230 229
240 236
244 242
253 245
SQ SEQUENCE 253 AA; 27004 MW; BD553B70BD55C6AD CRC64;
Query Match 5.2%; Score 13; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 6.8e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 198 GDSGGLVCGSVL 210
|||||
Db 206 GDSGGLVCGSVL 218
RESULT 3
URTG DESRO STANDARD; PRT; 394 AA.
ID AC P49150;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
gamma).
DE OS Desmodus rotundus (Vampire bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.

OX NCBI_TaxID=9430;
 RN (1)
 RP TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RL vampire bat *Desmodus rotundus*: cloning and expression.";
 RN Gene 105:229-237(1991).
 RP (2)
 RP CHARACTERIZATION.
 RX MEDLINE=9339059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of *Desmodus rotundus* (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: Probably essential to support the feeding habits of this
 CC exclusively haematophagous animal. Probable potent thrombolytic
 CC agent.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC
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 CC
 CC EMBL; M63990; AAA31595.1; -;
 CC PIR; J50600; J50600.
 CC HSSP; P98119; 1A51.
 CC MEROPS; S01.239; -;
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_SIA.
 CC Pfam; PF00051; kringle; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC ProDom; PD000395; Kringle; 1.
 CC SMART; SM00130; KR; 1.
 CC SMART; SM00020; Tryp_SPC; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS00070; KRINGLE_2; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
 FT DOMAIN 45 126 KRINGLE.
 FT DOMAIN 142 394
 FT ACT SITE 189 189 SERINE PROTEASE.
 FT ACT SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 45 126 BY SIMILARITY.
 FT DISULFID 66 108 BY SIMILARITY.
 FT DISULFID 97 121 BY SIMILARITY.
 FT DISULFID 131 262 BY SIMILARITY.
 FT DISULFID 174 190 BY SIMILARITY.
 FT DISULFID 182 251 BY SIMILARITY.
 FT DISULFID 276 351 BY SIMILARITY.
 FT DISULFID 308 324 BY SIMILARITY.

FT DISULFID 341 369 BY SIMILARITY.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 394 AA; 44105 MW; 9CCDF52F3D81FCD CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 194 DACQDGGGLVLC 206
 |||||
 Db 339 DACQDGGGLVLC 351
 RESULT 4
 URTB DESRO STANDARD; PRT; 431 AA.
 ID URTB DESRO STANDARD; PRT; 431 AA.
 AC P98121;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
 beta).
 OS *Desmodus rotundus* (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; *Desmodus*.
 OC NCBI_TaxID=9430;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat *Desmodus rotundus*: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN (2)
 RP CHARACTERIZATION.
 RX MEDLINE=9339059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of *Desmodus rotundus* (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: Probably essential to support the feeding habits of this
 CC exclusively haematophagous animal. Probable potent thrombolytic
 CC agent.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: Monomer.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC
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 CC
 CC EMBL; M63989; AAA31594.1; -;
 CC PIR; J50599; J50599.
 CC HSSP; P98119; 1A51.
 CC MEROPS; S01.239; -;
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_SIA.

```

DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; tryptsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
FT SIGNAL 1 36
FT CHAIN 37 431
FT DOMAIN 82 163
FT DOMAIN 179 431
FT ACT_SITE 226 226
FT ACT_SITE 275 275
FT ACT_SITE 382 382
FT DISULFID 41 52
FT DISULFID 46 63
FT DISULFID 65 74
FT DISULFID 82 163
FT DISULFID 103 145
FT DISULFID 134 158
FT DISULFID 168 299
FT DISULFID 211 227
FT DISULFID 219 288
FT DISULFID 313 388
FT DISULFID 345 361
FT DISULFID 378 406
FT CARBOHYD 139 139
FT CARBOHYD 352 352
SQ SEQUENCE 431 AA; 48221 MW; 6995B5675B162CBP CRC64;

Query Match 5.24; Score 13; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
DB 376 DACQDSGGPLVC 388

RESULT 5
TWSS_MOUSE STANDARD; PRT; 455 AA.
AC Q9ER04; Q9ER02; Q9ER03;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 5 (SC 3.4.21.-) (Spinesin).
GN TMPRSS5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning of mouse spinesin.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]_
SEQUENCE FROM N.A. (ISOFORM 4).

RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "Molecular cloning of mouse type 4 spinesin.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Name=4;
CC IsoId=Q9ER04-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q9ER04-2; Sequence=VSP_005397, VSP_005398;
CC Name=2;
CC IsoId=Q9ER04-3; Sequence=VSP_005395;
CC Name=3;
CC IsoId=Q9ER04-4; Sequence=VSP_005396;
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 SRCR domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AB016229; BAB20276.1; -
CC EMBL; AB016230; BAB20277.1; -
CC EMBL; AB016423; BAB20278.1; -
CC EMBL; AB041037; BAB40328.1; -
CC HSSP; P00763; IDPO.
CC MEROPS; S01.313; -.
CC MGD; MGI:1933407; Tmprss5.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR001190; Srcr_receptor.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS0240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC PROSITE; PS00420; SRCR_1; FALSE_NEG.
CC PROSITE; PS0287; SRCR_2; 1.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW Glycoprotein; Alternative splicing.
PT DOMAIN 1 49
PT TRANSMEM 50 70
FT CYTOPLASMIC (POTENTIAL),
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT SRCR.
FT DOMAIN 71 455
FT DOMAIN 112 207
FT DOMAIN 218 455
FT ACT_SITE 258 258
FT ACT_SITE 308 308
FT ACT_SITE 405 405
FT SITE 217 218
FT DISULFID 135 196
FT DISULFID 148 206
FT DISULFID 209 328
FT DISULFID 243 259
FT DISULFID 374 390
FT DISULFID 401 429
FT CARBOHYD 163 163
FT CARBOHYD 170 170
FT CARBOHYD 319 319
FT CARBOHYD 375 375
FT VARSPPLIC 1 144
FT VARSPPLIC 1 10
FT VARSPPLIC 1 182
FT VARSPPLIC 1 182
FT FTId=VSP_005395.
FT FTId=VSP_005396.
FT FTId=VSP_005397.
FT FTId=VSP_005397.

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FT VARSPLIC 183 192 GGLVPEAWKP -> MEAQVGLLV (in isoform 1).
FT FT CONFLICT 325 325 D -> G (IN REF. 1; BAB20277).
SQ SEQUENCE 455 AA; 49632 MW; 5CFC31789C6899AA CRC64;

Query Match 5.2%; Score 13; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVC 206
Db 399 DACQDSGGPLVC 411

RESULT 6
TMSS HUMAN
ID TMSS HUMAN STANDARD; PRT; 457 AA.
AC Q9H353;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN TMPSRS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX PubMed=11741986;
RA Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;
RT "Spinesin/TMPSRS5, a novel transmembrane serine protease, cloned from
human spinal cord.";
RL J. Biol. Chem. 277:6806-6812(2002).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in
neurons, in their axons, and at the synapses of motoneurons in the
spinal cord.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 SRCR domain.
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CC -----
DR EMBL; AB028140; BAB20375.1; -.
DR HSSP; P00763; IDPO.
DR Genew; HGNC:14908; TMPSRS5.
DR MIM; 606751; -.
DR MEROPS; S01.313; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srrc_receptor.
DR Pfam; PF00089; Srrc; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS02440; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00420; SRCR_1; FALSE NEG.
DR PROSITE; PS02287; SRCR_2; FALSE NEG.
KW Hydrolase; Serine protease; Transmembrane; Signal-anchor;
KW Glycoprotein.
FT DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT TRANSMEM 50 70
FT DOMAIN 71 457 EXTRACELLULAR (POTENTIAL).

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FT DOMAIN 112 207 SRCR.
FT ACT SITE 218 457 SERINE PROTEASE.
FT ACT SITE 258 457 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 308 457 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 405 457 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SITE 217 218 CLEAVAGE (POTENTIAL).
FT SITE 217 218 BY SIMILARITY.
FT DISULFID 135 196 BY SIMILARITY.
FT DISULFID 148 206 BY SIMILARITY.
FT DISULFID 209 328 BY SIMILARITY.
FT DISULFID 243 259 BY SIMILARITY.
FT DISULFID 374 390 BY SIMILARITY.
FT DISULFID 401 429 BY SIMILARITY.
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 319 319 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 457 AA; 49574 MW; 64406AB4985A2651 CRC64;

Query Match 5.2%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVC 206
Db 399 DACQDSGGPLVC 411

RESULT 7
URTL DESRO
ID URTL DESRO STANDARD; PRT; 477 AA.
AC P98139;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
alpha-1).
OS Desmodus rotundus (Vampire bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.
OX NCBI_TaxID=9430;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=92039036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
RL Gene 105:229-237(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93393059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RC TISSUE=Salivary gland;
RX MEDLINE=98022741; PubMed=9354616;
RA Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
Schleuning W.D., Bode W.;
RT "Catalytic domain structure of vampire bat plasminogen activator: a
molecular paradigm for proteolysis without activation cleavage.";
RL Biochemistry 36:13483-13493(1997).
CC -!- FUNCTION: Probably essential to support the feeding habits of this
exclusively haematophagous animal. Potent thrombolytic agent.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.

```

CC -|- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 CC the presence of fibrin I.
 CC -|- SUBUNIT: Monomer.
 CC -|- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 CC and the kringle domain apparently mediates fibrin-induced
 CC stimulation of activity.
 CC -|- SIMILARITY: Belongs to peptidase family S1.
 CC -|- SIMILARITY: Contains 1 EGF-like domain.
 CC -|- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -|- SIMILARITY: Contains 1 kringle domain.
 CC -----
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 CC -----
 CC EMBL; M63987; AAA31591.1; -;
 CC EMBL; M63986; AAA31592.1; -;
 CC PIR; JS0597; JS0597.
 CC PDB; 1A51; 23-MAR-99.
 CC MEROPS; S01.212; -;
 CC GlycoSuiteDB; P98119; -;
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR000083; Fibnctn1.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00008; EGF; 1.
 CC Pfam; PF00039; fn1; 1.
 CC Pfam; PF00051; kringle; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC ProDom; PD000395; Kringle; 1.
 CC SMART; SM00181; EGF; 1.
 CC SMART; SM00058; FN1; 1.
 CC SMART; SM00130; KR; 1.
 CC SMART; SM00020; TRYP_SPC; 1.
 CC PROSITE; PS00022; EGF_1; 1.
 CC PROSITE; PS01186; EGF_2; 1.
 CC PROSITE; PS00026; EGF_3; 1.
 CC PROSITE; PS01253; FIBRONECTIN_1; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS00070; KRINGLE_2; 1.
 CC PROSITE; PS00240; TRYPSIN_DOM; 1.
 CC PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC PROSITE; PS00135; TRYPSIN_SER; 1.
 CC Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family; 3D-structure.
 FT SIGNAL 1 36
 FT CHAIN 37 477 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1.
 FT DOMAIN 40 82 FIBRONECTIN TYPE-I.
 FT DOMAIN 83 121 EGF-LIKE.
 FT DOMAIN 128 209 KRINGLE.
 FT DOMAIN 225 477 SERINE PROTEASE.
 FT ACT_SITE 272 272 CHARGE RELAY SYSTEM.
 FT ACT_SITE 321 321 CHARGE RELAY SYSTEM.
 FT ACT_SITE 428 428 CHARGE RELAY SYSTEM.
 FT DISULFID 42 72 BY SIMILARITY.
 FT DISULFID 70 79 BY SIMILARITY.
 FT DISULFID 87 98 BY SIMILARITY.
 FT DISULFID 92 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 128 209 BY SIMILARITY.
 FT DISULFID 149 191 BY SIMILARITY.
 FT DISULFID 180 204 BY SIMILARITY.
 FT DISULFID 214 345 BY SIMILARITY.
 FT DISULFID 257 273

FT DISULFID 265 334
 FT DISULFID 359 434
 FT DISULFID 391 407
 FT DISULFID 424 452
 FT CARBOHYD 153 153
 FT CARBOHYD 398 398
 FT TURN 214 215
 FT STRAND 223 224
 FT TURN 226 227
 FT STRAND 230 231
 FT HELIX 234 236
 FT TURN 238 239
 FT STRAND 240 245
 FT STRAND 254 263
 FT TURN 264 265
 FT STRAND 266 269
 FT HELIX 271 273
 FT TURN 280 282
 FT STRAND 284 287
 FT TURN 297 298
 FT STRAND 300 309
 FT TURN 311 312
 FT TURN 315 317
 FT TURN 319 320
 FT STRAND 323 328
 FT STRAND 338 338
 FT TURN 339 340
 FT STRAND 341 341
 FT STRAND 345 345
 FT TURN 349 350
 FT TURN 355 356
 FT STRAND 358 363
 FT STRAND 366 366
 FT STRAND 374 374
 FT STRAND 379 385
 FT HELIX 388 390
 FT TURN 393 398
 FT TURN 403 404
 FT STRAND 405 409
 FT TURN 425 426
 FT TURN 428 429
 FT STRAND 431 436
 FT TURN 437 438
 FT STRAND 439 448
 FT TURN 455 456
 FT STRAND 459 463
 FT HELIX 464 467
 FT HELIX 468 474
 SQ SEQUENCE 477 AA; 53616 MW; AA06FD1739C1085E CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred.No.1.2e-05; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 194 DACQSDSGGPLVC 206
 DB 422 DACQSDSGGPLVC 434
 RESULT 8
 ID UR2 DESRO STANDARD; PRT; 477 AA.
 AC P15638;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA
 DE alpha-2) (BAT-PA) (T-plasminogen activator).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;

Desmodontinae; Desmodus.
 NCBI_TaxID=9430;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Salivary gland;
 MEDLINE=92039036; PubMed=137019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 vampire bat Desmodus rotundus: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Salivary gland;
 RX MEDLINE=90036867; PubMed=2509450;
 RA Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
 Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
 RT "Isolation, characterization, and cDNA cloning of a vampire bat
 salivary plasminogen activator.";
 RL J. Biol. Chem. 264:17947-17952(1989).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 Donner P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: Probably essential to support the feeding habits of this
 CC exclusively haematophagous animal. Probable potent thrombolytic
 CC agent.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-val bond in
 CC plasminogen to form plasmin.
 CC -!- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 CC the presence of fibrin I.
 CC -!- SUBUNIT: Monomer.
 CC -!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 CC and the kringle domain apparently mediates fibrin-induced
 CC stimulation of activity.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M63988; AAA31593.1; -;
 CC EMBL; J05082; AAA31596.1; -;
 CC PIR; A34369; A34369.
 CC PIR; J50598; J50598.
 CC HSSP; P98119; IAS1.
 CC
 CC MEROPS; S01.232; -;
 CC InterPro; IPR009003; Cys Ser trypsin.
 CC InterPro; IPR006209; EGF-like.
 CC InterPro; IPR000083; Fibronectin.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001254; Peptidase S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC Pfam; PF00008; EGF; 1.
 CC Pfam; PF00039; fni; 1.
 CC Pfam; PF00051; kringle; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC ProDom; PD000395; Kringle; 1.

DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TYPD_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 477 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 2.
 FT DOMAIN 40 82 FIBRONECTIN TYPE-I.
 FT DOMAIN 83 121 EGF-LIKE.
 FT DOMAIN 128 209 KRINGLE.
 FT DOMAIN 225 477 SERINE PROTEASE.
 FT ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 321 321 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 428 428 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 42 72 BY SIMILARITY.
 FT DISULFID 70 79 BY SIMILARITY.
 FT DISULFID 87 98 BY SIMILARITY.
 FT DISULFID 92 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 128 209 BY SIMILARITY.
 FT DISULFID 149 191 BY SIMILARITY.
 FT DISULFID 180 204 BY SIMILARITY.
 FT DISULFID 214 345 BY SIMILARITY.
 FT DISULFID 257 273 BY SIMILARITY.
 FT DISULFID 265 334 BY SIMILARITY.
 FT DISULFID 359 434 BY SIMILARITY.
 FT DISULFID 391 407 BY SIMILARITY.
 FT DISULFID 424 452 BY SIMILARITY.
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 403 403 N -> K (IN REF. 2).
 FT CONFLICT 417 417 Y -> H (IN REF. 2).
 FT CONFLICT 435 435 M -> R (IN REF. 2).
 SQ SEQUENCE 477 AA; 53719 MW; 17486555C0E5077C CRC64;
 Query Match 5.2%; Score 13; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 194 DACQDSGGPLVC 206
 |||||
 Db 422 DACQDSGGPLVC 434
 RESULT 9
 TPA MOUSE
 ID TPA MOUSE STANDARD; PRT; 559 AA.
 AC P11214; Q91VP2;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator).
 GN PLAT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8808703; PubMed=2826484;
 RA Rickles R.J., Darrow A.L., Strickland S.;
 RT "Molecular cloning of complementary DNA to mouse tissue plasminogen

RT activator mRNA and its expression during P9 teratocarcinoma cell
 RT differentiation";
 RL J. Biol. Chem. 263:1563-1569 (1988).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Wagner L., Schenker C.M., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Haeberle C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Ustin T.B., Tothivuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
 CC to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
 CC controlling plasmin-mediated proteolysis, it plays an important
 CC role in tissue remodeling and degradation, in cell migration and
 CC many other physiopathological events.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -1- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
 CC bond.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular.
 CC -1- PFM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 CC ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC -1- MISCELLANEOUS: Binds to the kringle structure of the fibrin A
 CC chain. Binding to fibrin enhances its catalytic activity.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -1- SIMILARITY: Contains 2 kringle domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J03520; AAA04070.1; -;
 DR EMBL; BC011256; AAH11256.1; -;
 DR PIR; A29941; A29941.
 DR HGSP; P00750; 1A5H.
 DR MEROPS; S01.232; -;
 DR MGD; MGI:97610; Plat.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000083; Fibrinctnl.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00039; fn1; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.
 DR PRODom; PD000395; Kringle; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS01253; KRINGLE_1; 2.
 DR PROSITE; PS00021; KRINGLE_2; 2.
 DR PROSITE; PS00070; KRINGLE_3; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Plasma; Kringle; EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 17 PROBABLE.
 FT PROPEP 18 29
 FT CHAIN 30 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR.
 FT CHAIN 30 308 TISSUE-TYPE PLASMINOGEN ACTIVATOR A
 FT CHAIN 309 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR B
 FT CHAIN 36 78 FIBRONECTIN TYPE-1.
 FT DOMAIN 79 117 EGF-LIKE.
 FT DOMAIN 124 205 KRINGLE 1.
 FT DOMAIN 213 294 KRINGLE 2.
 FT DOMAIN 309 559 SERINE PROTEASE.
 FT ACT_SITE 355 355 CHARGE RELAY SYSTEM.
 FT ACT_SITE 404 404 CHARGE RELAY SYSTEM.
 FT ACT_SITE 510 510 CHARGE RELAY SYSTEM.
 FT DISULFID 38 68 BY SIMILARITY.
 FT DISULFID 66 75 BY SIMILARITY.
 FT DISULFID 83 94 BY SIMILARITY.
 FT DISULFID 88 105 BY SIMILARITY.
 FT DISULFID 107 116 BY SIMILARITY.
 FT DISULFID 124 205 BY SIMILARITY.
 FT DISULFID 145 187 BY SIMILARITY.
 FT DISULFID 176 200 BY SIMILARITY.
 FT DISULFID 213 294 BY SIMILARITY.
 FT DISULFID 234 276 BY SIMILARITY.
 FT DISULFID 265 289 BY SIMILARITY.
 FT DISULFID 297 428 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 340 356 BY SIMILARITY.
 FT DISULFID 348 417 BY SIMILARITY.
 FT DISULFID 442 516 BY SIMILARITY.
 FT DISULFID 474 490 BY SIMILARITY.
 FT DISULFID 506 534 BY SIMILARITY.
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 260 260 G -> A (IN REF. 1).
 FT CONFLICT 325 325 P -> A (IN REF. 1).
 SQ SEQUENCE 559 AA; 63122 MW; 8CCB2BDB94514D9 CRC64;

Query Match 5.2%; Score 13; DB 1; Length 559;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDGGGGLVC 206
 Db 504 DACQDGGGGLVC 516
 |||||

RESULT 10
 TPA_RAT STANDARD; PRT; 559 AA.
 ID_TPA_RAT
 AC P19637;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator).

DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DB Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
 GN PLAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Melanoma;
 RX MEDLINE=83115262; PubMed=6337343;
 RA Pennica D., Holmes W.E., Kohr W.D., Harkins R.N., Vohar G.A.,
 RA Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
 RA Goeddel D.V., Collen D.;
 RT "Cloning and expression of human tissue-type plasminogen activator
 RT cDNA in E. coli.";
 RL Nature 301:214-221(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal lung;
 RX MEDLINE=88262579; PubMed=3133640;
 RA Sasaki H., Saito Y., Hayaashi M., Otsuka K., Niwa M.;
 RT "Nucleotide sequence of the tissue-type plasminogen activator cDNA
 RT from human fetal lung cells.";
 RL Nucleic Acids Res. 16:5695-5695(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88054470; PubMed=2824147;
 RA Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
 RA Hsiung N.;
 RT "Expression of human uterine tissue-type plasminogen activator in
 RT mouse cells using BPV vectors.";
 RL DNA 6:461-472(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86196143; PubMed=3009482;
 RA Friesner Degen S.J., Rajput B., Reich E.;
 RT "The human tissue plasminogen activator gene.";
 RL J. Biol. Chem. 261:6972-6985(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84298137; PubMed=6089198;
 RA Ny T., Elgh F., Lund B.;
 RT "The structure of the human tissue-type plasminogen activator gene:
 RT correlation of intron and exon structures to functional and
 RT structural domains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86284200; PubMed=3090401;
 RA Harris T.J., Patel T., Marston P.A., Little S., Emtage J.S.,
 RA Ondenakker G., Volckaert G., Rombauts W., Billiau A., Smer P.;
 RT "Cloning of cDNA coding for human tissue-type plasminogen activator
 RT and its expression in Escherichia coli.";
 RL Mol. Biol. Med. 3:279-292(1986).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM SHORT).
 RC TISSUE=umbilical vein;
 RX MEDLINE=90192129; PubMed=2107528;
 RA Siebert P.D., Fong K.;
 RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
 RT human endothelial cells.";
 RL Nucleic Acids Res. 18:1086-1086(1990).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Caevant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [9]
 RP SEQUENCE OF 212-361 FROM N.A.
 RX MEDLINE=83169656; PubMed=6572897;
 RA Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
 RA Josephson S.;
 RT "Isolation of cDNA sequences coding for a part of human tissue
 RT plasminogen activator.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
 RN [10]
 RP SEQUENCE OF 1-36 FROM N.A.
 RX MEDLINE=85289338; PubMed=3161893;
 RA Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
 RA Schleuning W.-D.;
 RT "Isolation and characterization of the human tissue-type plasminogen
 RT activator structural gene including its 5' flanking region.";
 RL J. Biol. Chem. 260:11223-11230(1985).
 RN [11]
 RP SEQUENCE OF 31-562 FROM N.A.
 RX MEDLINE=91291340; PubMed=1368681;
 RA Itagaki Y., Yasuda H., Morinaga T., Mitsuoka S., Higashio K.;
 RT "Purification and characterization of tissue plasminogen activator
 RT secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
 RL Agric. Biol. Chem. 55:1225-1232(1991).
 RN [12]
 RP SEQUENCE OF 36-562.
 RC TISSUE=Melanoma;
 RX MEDLINE=85000468; PubMed=6433976;
 RA Pohl G., Kællström M., Bergsdorf N., Wallen P., Joernvall H.;
 RT "Tissue plasminogen activator: peptide analyses confirm an indirectly
 RT derived amino acid sequence, identify the active site serine residue,
 RT establish glycosylation sites, and localize variant differences.";
 RL Biochemistry 23:3701-3707(1984).
 RN [13]
 RP SEQUENCE OF 33-52 AND 311-330.
 RC TISSUE=Melanoma;
 RX MEDLINE=83209620; PubMed=6682760;
 RA Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.;
 RT "Purification and characterization of a melanoma cell plasminogen
 RT activator.";
 RL Eur. J. Biochem. 132:681-686(1983).
 RN [14]
 RP STRUCTURE OF CARBOHYDRATES.
 RX MEDLINE=90092112; PubMed=2513186;
 RA Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
 RT "Carbohydrate structure of recombinant human uterine tissue
 RT plasminogen activator expressed in mouse epithelial cells.";
 RL Eur. J. Biochem. 186:273-286(1989).
 RN [15]
 RP CARBOHYDRATE-LINKAGE SITE THR-96.
 RX MEDLINE=91159408; PubMed=1900431;
 RA Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
 RT "Tissue plasminogen activator has an O-linked fucose attached to
 RT threonine-61 in the epidermal growth factor domain.";
 RL Biochemistry 30:2311-2314(1991).
 RN [16]
 RP DISULFIDE BONDS IN KRINGLE 2.
 RX MEDLINE=91244765; PubMed=1645336;

RA Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
 RT "Disulfide pairing of the recombinant kringle-2 domain of tissue
 RL plasminogen activator produced in *Escherichia coli*.";
 RN J. Biol. Chem. 266:10070-10072(1991).
 RP [17]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
 RX MEDLINE=96200985; PubMed=8613982;
 RA Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
 RA Bode W.;
 RT "The 2.3 A crystal structure of the catalytic domain of recombinant
 RL two-chain human tissue-type plasminogen activator.";
 RN J. Mol. Biol. 258:117-135(1996).
 RP [18]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
 RX MEDLINE=97449126; PubMed=9305622;
 RA Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
 RA Bode W.;
 RT "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
 RL crystal structure of single-chain human tPA.";
 RN EMBO J. 16:4797-4805(1997).
 RP [19]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
 RX MEDLINE=92111803; PubMed=1310033;
 RA de Vos A., Uitsch M.H., Kelley R.F., Padmanabhan K., Tulinsky A.,
 RA Westbrook M.L., Kossiakof A.A.;
 RT "Crystal structure of the kringle 2 domain of tissue plasminogen
 RL activator at 2.4-A resolution.";
 RN Biochemistry 31:270-279(1992).
 RP [20]
 RP STRUCTURE BY NMR OF KRINGLE 2.
 RX MEDLINE=90122799; PubMed=2558718;
 RA Byeon I.-J.L., Kelley R.F., Llinas M.;
 RT "1H NMR structural characterization of a recombinant kringle 2 domain
 RL from human tissue-type plasminogen activator.";
 RN Biochemistry 28:9350-9360(1989).
 RP [21]
 RP STRUCTURE BY NMR OF KRINGLE 2.
 RX MEDLINE=91200042; PubMed=1901789;
 RA Byeon I.-J.L., Kelley R.F., Llinas M.;
 RT "Kringle-2 domain of the tissue-type plasminogen activator. 1H-NMR
 RL assignments and secondary structure.";
 RN Eur. J. Biochem. 197:155-165(1991).
 RP [22]
 RP STRUCTURE BY NMR OF KRINGLE 2.
 RX MEDLINE=92106329; PubMed=1762144;
 RA Byeon I.-J.L., Llinas M.;
 RT "Solution structure of the tissue-type plasminogen activator kringle
 RL 2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
 drug.";
 RN J. Mol. Biol. 222:1035-1051(1991).
 RP [23]

Query Match 5.2%; Score 13; DB 1; Length 562;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 194 DACQDSGGPLVC 206
 Db 507 DACQDSGGPLVC 519
 |||||
 |||||

RESULT 12
 TPA BOVIN
 ID TPA BOVIN STANDARD; PRT; 566 AA.
 AC Q26198;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator).
 GN PLAT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI TaxID=9913;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RA Ravn P., Berglund L., Petersen T.B.;
 RT "Cloning and characterization of the bovine plasminogen activators uPA
 RL and tPA.";
 RL Int. Dairy J. 5:605-617(1995).
 CC -!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
 CC to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
 CC controlling plasmin-mediated proteolysis, it plays an important
 CC role in tissue remodeling and degradation, in cell migration and
 CC many other physiopathological events.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
 CC bond.
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular.
 CC -!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 CC ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC -!- MISCELLANEOUS: Binds to the kringle structure of the fibrin A
 CC chain. Binding to fibrin enhances its catalytic activity.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -!- SIMILARITY: Contains 2 kringle domains.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X85800; CAA59795.1; -.
 DR HSSP; P00750; IRTF.
 DR MEROPS; S01_232; -.
 DR InterPro; IPR005903; Cys Ser trypsin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR000083; Fibrinctnl.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00039; fnl; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW plasma; Kringle; EGF-like domain; Repeat; Signal.
 GN SIGNAL 1 21 BY SIMILARITY.
 FT PROPEP 22 33
 FT CHAIN 34 566 TISSUE-TYPE PLASMINOGEN ACTIVATOR.

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FT CHAIN 34 314 TISSUE-TYPE PLASMINOGEN ACTIVATOR A
FT CHAIN 315 566 TISSUE-TYPE PLASMINOGEN ACTIVATOR B
FT CHAIN 315 566 CHAIN
FT DOMAIN 40 82 FIBRONECTIN TYPE-I.
FT DOMAIN 83 121 EGF-LIKE.
FT DOMAIN 128 209 KRINGLE 1.
FT DOMAIN 219 300 KRINGLE 2.
FT DOMAIN 315 566 SERINE PROTEASE.
FT ACT SITE 361 361 CHARGE RELAY SYSTEM.
FT ACT SITE 410 410 CHARGE RELAY SYSTEM.
FT ACT SITE 517 517 CHARGE RELAY SYSTEM.
FT DISULFID 42 72 BY SIMILARITY.
FT DISULFID 70 79 BY SIMILARITY.
FT DISULFID 87 98 BY SIMILARITY.
FT DISULFID 92 109 BY SIMILARITY.
FT DISULFID 111 120 BY SIMILARITY.
FT DISULFID 128 209 BY SIMILARITY.
FT DISULFID 149 191 BY SIMILARITY.
FT DISULFID 180 204 BY SIMILARITY.
FT DISULFID 219 300 BY SIMILARITY.
FT DISULFID 240 282 BY SIMILARITY.
FT DISULFID 271 295 BY SIMILARITY.
FT DISULFID 303 434 INTERCHAIN (BY SIMILARITY).
FT DISULFID 346 362 BY SIMILARITY.
FT DISULFID 354 423 BY SIMILARITY.
FT DISULFID 448 523 BY SIMILARITY.
FT DISULFID 480 496 BY SIMILARITY.
FT DISULFID 513 541 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 566 AA; 63701 MW; 2866BEB4E32276C3 CRC64;

Query Match 5.2%; Score 13; DB 1; Length 566;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACGDSGGPLVC 206
Db 511 DACGDSGGPLVC 523

RESULT 13
FAL2_BOVIN
ID FAL2_BOVIN STANDARD; PRT; 593 AA.
AC P98140;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAF) (Fragment).
GN F12.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN TISSUE=Liver;
RC TISSUE=Liver;
RX MEDLINE=94242782; PubMed=8186251;
RA Shibuya Y., Samba U., Okabe H., Kambara T., Yamamoto T.;
RT "Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human and guinea pig molecules.";
RL Biochim. Biophys. Acta 1206:63-70(1994).
RN [2]
RN SEQUENCE OF 10-21; 350-364 AND 525-550.
RP MEDLINE=77182112; PubMed=861210;
RA Fujikawa K., Walsh A.K., Davie W.B.;
RT "Isolation and characterization of bovine factor XII (Hageman factor).";
RL Biochemistry 16:2270-2278(1977).
CC -1- FUNCTION: Factor XII is a serum glycoprotein that participates in

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CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
CC VII to form factor VIIa and factor XI to form factor XIIa.
CC -1- PTM: O- AND N-GLYCOSYLATED (BY SIMILARITY).
CC -1- MISCELLANEOUS: Factor XII, prekallikrein, and HMM kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
CC XIIa activates factor XI to factor XIa. Bovine factor XII is
CC cleaved only to alpha-factor XIIa as it lacks the trypsin/
CC kallikrein cleavage site.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 1 fibronectin type I domain.
CC -1- SIMILARITY: Contains 1 fibronectin type II domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S70164; AAB30804.2; -.
CC PIR; S45281; S45281.
CC HSP; P00763; 1DPO.
CC MEROPS; S01.211; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR000083; Fibrinctnl.
CC InterPro; IPR000562; FN Type II.
CC InterPro; IPR006210; tEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00040; fn2; 1.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000995; FN Type II; 1.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00181; EGF; 2.
CC SMART; SM00058; FN1; 1.
CC SMART; SM00059; FN2; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PSS0026; EGF_3; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS50070; KRINGLE_2; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
KW Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
FT NON_TER 1 1
FT SIGNAL <1 9 POTENTIAL..
FT CHAIN 10 349 ALPHA-FACTOR XIIA HEAVY CHAIN.
FT CHAIN 350 593 ALPHA-FACTOR XIIA LIGHT CHAIN.
FT DOMAIN 37 78 FIBRONECTIN TYPE-II.
FT DOMAIN 84 121 EGF-LIKE 1.
FT DOMAIN 123 163 FIBRONECTIN TYPE-I.
FT DOMAIN 164 200 EGF-LIKE 2.

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FT DOMAIN 207 287 KRINGLE.
FT DOMAIN 237 333 PRO-RICH.
FT ACT SITE 350 399 SERINE PROTEASE.
FT ACT SITE 389 438 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 438 438 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 541 541 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 88 100 BY SIMILARITY.
FT DISULFID 94 109 BY SIMILARITY.
FT DISULFID 111 120 BY SIMILARITY.
FT DISULFID 125 153 BY SIMILARITY.
FT DISULFID 151 160 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 173 188 BY SIMILARITY.
FT DISULFID 190 199 BY SIMILARITY.
FT DISULFID 207 287 BY SIMILARITY.
FT DISULFID 230 262 BY SIMILARITY.
FT DISULFID 258 282 BY SIMILARITY.
FT DISULFID 336 463 BY SIMILARITY.
FT DISULFID 374 390 BY SIMILARITY.
FT DISULFID 382 452 BY SIMILARITY.
FT DISULFID 413 416 BY SIMILARITY.
FT DISULFID 479 547 BY SIMILARITY.
FT DISULFID 510 526 BY SIMILARITY.
FT DISULFID 537 568 BY SIMILARITY.
FT CARBOHYD 99 99 O-LINKED (PUC) (BY SIMILARITY).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 263 263 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 410 410 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 593 AA; 65148 MW; 721592BA792BD61F CRC64;

Query Match 5.2%; Score 13; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.5e-05; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 194 DACQDSGGPLVC 206
Db 535 DACQDSGGPLVC 547

RESULT 14
FA12 CAVPO STANDARD; PRT; 603 AA.
AC Q04962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor [EC 3.4.21.38] (Hageman factor)
DE (HAF) (Fragment).
GN P12
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332 AND 359-373.
RC TISSUE=Liver;
RX MEDLINE=93003367; PubMed=1390917;
RA Semba U., Yamamoto T., Kunisada T., Shibuya Y., Tanase S.,
RA Kambara T., Okabe H.;
RT "Primary structure of guinea-pig Hageman factor: sequence around the
RT cleavage site differs from the human molecule.";
RL Biochim. Biophys. Acta 1159:113-121(1992).
CC -!- FUNCTION: Factor XII is a serum glycoprotein that participates in
CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
CC VII to form factor VIIa and factor XI to form factor Xla.
CC -!- MISCELLANEOUS: Factor XII, prekallikrein, and HNW kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor Xla and then to beta-factor Xlaa. Alpha-factor
CC Xlaa activates factor XI to factor Xla.
CC -!- SIMILARITY: Belongs to peptidase family S1.

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CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X68615; CAA48600.1; -.
DR PIR; S28941; S28941.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.211; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; FibrinctnI.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1a.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00013; FN1YPE11.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000995; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
KW Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
FT NON_TER 1 1
FT SIGNAL <1 18
FT CHAIN 19 358 ALPHA-FACTOR XIIA HEAVY CHAIN.
FT CHAIN 359 603 ALPHA-FACTOR XIIA LIGHT CHAIN.
FT DOMAIN 46 87 FIBRONECTIN TYPE-II.
FT DOMAIN 93 130 EGF-LIKE 1.
FT DOMAIN 132 172 FIBRONECTIN TYPE-I.
FT DOMAIN 173 209 EGF-LIKE 2.
FT DOMAIN 216 294 KRINGLE.
FT DOMAIN 312 342 PRO-RICH.
FT DOMAIN 359 603 SERINE PROTEASE.
FT ACT_SITE 338 398 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 447 447 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 551 551 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 37 109 BY SIMILARITY.
FT DISULFID 103 118 BY SIMILARITY.
FT DISULFID 120 129 BY SIMILARITY.
FT DISULFID 134 162 BY SIMILARITY.
FT DISULFID 160 169 BY SIMILARITY.

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FT DISULFID 177 188 BY SIMILARITY.
 FT DISULFID 182 197 BY SIMILARITY.
 FT DISULFID 199 208 BY SIMILARITY.
 FT DISULFID 216 294 BY SIMILARITY.
 FT DISULFID 237 276 BY SIMILARITY.
 FT DISULFID 265 289 BY SIMILARITY.
 FT DISULFID 345 472 BY SIMILARITY.
 FT DISULFID 383 399 BY SIMILARITY.
 FT DISULFID 391 461 BY SIMILARITY.
 FT DISULFID 422 425 BY SIMILARITY.
 FT DISULFID 488 557 BY SIMILARITY.
 FT DISULFID 520 536 BY SIMILARITY.
 FT DISULFID 547 578 BY SIMILARITY.
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 603 AA; 66795 MW; 48DC6B946FB9ED59 CRC64;

Query Match 5.2%; Score 13; DB 1; Length 603;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVC 206
 Db 545 DACQDSGGPLVC 557

RESULT 15
 PAL2 HUMAN
 ID -PAL2_HUMAN STANDARD; PRT; 615 AA.
 AC P00748; P78339;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor) (HAF).
 GN P12.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88007593; PubMed=2888762;
 RA Cool D.E., McGillivray R.T.A.;
 RT "Characterization of the human blood coagulation factor XII gene.
 RT Intron/exon gene organization and analysis of the 5'-flanking
 RT region.";
 RL J. Biol. Chem. 262:13662-13673(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.
 RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
 RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (AUG-2002) to the ENBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 4-615 FROM N.A.
 RX MEDLINE=8616794; PubMed=3754331;
 RA Tripodi M., Citarella F., Guida S., Galeffi P., Pantoni A.,
 RA Cortese R.;
 RT "cDNA sequence coding for human coagulation factor XII (Hageman).";
 RL Nucleic Acids Res. 14:3146-3146(1986).
 RN [4]
 RP SEQUENCE OF 14-615 FROM N.A.
 RX MEDLINE=86033830; PubMed=3877053;
 RA Cool D.E., Edgell C.-J.S., Louie G.V., Zollner M.J., Brayer G.D.,
 RA McGillivray R.T.A.;
 RT "Characterization of human blood coagulation factor XII cDNA.
 RT Prediction of the primary structure of factor XII and the tertiary
 RT structure of beta-factor XIIa.";
 RL J. Biol. Chem. 260:13666-13676(1985).
 RN [5]
 RP SEQUENCE OF 146-615 FROM N.A.
 RX MEDLINE=86216049; PubMed=3011063;

RA Que B.G., Davie E.W.;
 RT "Characterization of a cDNA coding for human factor XII (Hageman
 RT factor).";
 RL Biochemistry 25:1525-1528(1986).
 RN [6]
 RP SEQUENCE OF 20-379.
 RX MEDLINE=85182674; PubMed=3886654;
 RA McMullen B.A., Fujikawa K.;
 RT "Amino acid sequence of the heavy chain of human alpha-factor XIIa
 RT (activated Hageman factor).";
 RL J. Biol. Chem. 260:5328-5341(1985).
 RN [7]
 RP SEQUENCE OF 354-362 AND 373-615.
 RX MEDLINE=83291041; PubMed=6604055;
 RA Fujikawa K., McMullen B.A.;
 RT "Amino acid sequence of human beta-factor XIIa.";
 RL J. Biol. Chem. 258:10924-10933(1983).
 RN [8]
 RP SEQUENCE OF 561-615 FROM N.A.
 RT TISSUE=Blood;
 RX MEDLINE=96133302; PubMed=8528215;
 RA Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel W.;
 RT "The novel acceptor splice site mutation 11396(G-->A) in the factor
 RT XII gene causes a truncated transcript in cross-reacting material
 RT negative patients.";
 RL Hum. Mol. Genet. 4:1235-1237(1995).
 RN [9]
 RP CARBOHYDRATE-LINKAGE SITE THR-109.
 RX MEDLINE=92184750; PubMed=1544894;
 RA Harris R.J., Ling V.T., Spellman M.W.;
 RT "O-linked fucose is present in the first epidermal growth factor
 RT domain of factor XII but not protein C.";
 RL J. Biol. Chem. 267:5102-5107(1992).
 RN [10]
 RP VARIANT WASHINGTON D.C. SER-590.
 RX MEDLINE=90046788; PubMed=2510163;
 RA Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
 RA Saito H.;
 RT "Coagulation factor XII (Hageman factor) Washington D.C.: inactive
 RT factor XIIa results from Cys-571-->Ser substitution.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
 RN [11]
 RP VARIANT LOCARNO PRO-372.
 RX MEDLINE=94325559; PubMed=8049433;
 RA Hovinga J.K., Schaller J., Stricker H., Willemin W.A., Furlan M.,
 RA Laemmle B.;
 RT "Coagulation factor XII Locarno: the functional defect is caused by
 RT the amino acid substitution Arg-353-->Pro leading to loss of a
 RT kallikrein cleavage site.";
 RL Blood 84:1173-1181(1994).
 RN [12]
 RP VARIANT TENRI CYS-53.
 RX MEDLINE=99290785; PubMed=10361128;
 RA Kondo S., Tokunaga P., Kawano S., Oono Y., Kumagai S., Koide T.;
 RT "Factor XII Tenri, a novel cross-reacting material negative factor XII
 RT deficiency, occurs through a protease-mediated degradation.";
 RL Blood 93:4300-4308(1999).
 CC -1- FUNCTION: Factor XII is a serum glycoprotein that participates in
 CC the initiation of blood coagulation, fibrinolysis, and the
 CC generation of bradykinin and angiotensin.
 CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
 CC VII to form factor VIIa and factor XI to form factor Xla.
 CC -1- PTM: O- AND N-GLYCOSYLATED.
 CC -1- DISEASE: Defects in F12 do not cause any clinical symptoms. The
 CC sole effect is that whole-blood clotting time is prolonged.
 CC -1- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
 CC complex bound to an anionic surface. Prekallikrein is cleaved by
 CC factor XII to form kallikrein, which then cleaves factor XII first
 CC to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
 CC XIIa activates factor XI to factor Xla.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 fibronectin type I domain.

CC CC -1- SIMILARITY: Contains 1 fibronectin type II domain.
 CC CC -1- SIMILARITY: Contains 1 kringle domain.
 CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC CC modified and this statement is not removed. Usage by and for commercial
 CC CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC CC or send an email to license@isb-sib.ch).
 CC CC -----
 CC EMBL: M31315; AAB70225.1; --
 CC EMBL: AF538691; AAM97932.1; --
 CC EMBL: M11723; AAB51986.1; --
 CC EMBL: M17466; AAB59490.1; --
 CC EMBL: M17464; AAB59490.1; JOINED.
 CC EMBL: M17465; AAB59490.1; JOINED.
 CC EMBL: M13147; AAB70224.1; --
 CC EMBL: U71274; AAB51203.1; --
 CC FIR: A29411; KFHU12.
 CC HSSP: P00763; LDPO.
 CC MEROPS: S01.211; --
 CC Genew: HGNC:3530; F12.
 CC MIM: 234000; --
 CC GO: GO:0003805; F: blood coagulation factor XI activity; TAS.
 CC GO: GO:0003806; F: blood coagulation factor XII activity; TAS.
 CC GO: GO:0008236; F: serine-type peptidase activity; TAS.
 CC GO: GO:0007596; P: blood coagulation; TAS.
 CC InterPro: IPR009003; Cys Ser trypsin.
 CC InterPro: IPR006209; EGF-like
 CC InterPro: IPR000083; Fibrinctn1.
 CC InterPro: IPR000562; FN_Type_II.
 CC InterPro: IPR006210; IEFG.
 CC InterPro: IPR000001; Kringle.
 CC InterPro: IPR001254; Peptidase S1.
 CC InterPro: IPR001314; Peptidase_S1A.
 CC Pfam: PF00008; EGF; 2.
 CC Pfam: PF00039; fnl; 1.
 CC Pfam: PF00040; fn2; 1.
 CC Pfam: PF00051; kringle; 1.
 CC Pfam: PF00089; trypsin; 1.
 CC PRINTS: PR00722; CHYMOTRYPSIN.
 CC PRINTS: PR00013; FNTPEII.
 CC PRINTS: PR00018; KRINGLE.
 CC ProDom: PD000995; FN_Type_II; 1.
 CC ProDom: PD000395; Kringle; 1.
 CC SMART: SM00181; EGF; 2.
 CC SMART: SM00059; FNL; 1.
 CC SMART: SM00059; FN2; 1.
 CC SMART: SM00130; KR; 1.
 CC SMART: SM00020; Tryp_SPC; 1.
 CC PROSITE: PS00022; EGF_1; 2.
 CC PROSITE: PS01186; EGF_2; 1.
 CC PROSITE: PS50026; EGF_3; 2.
 CC PROSITE: PS01253; FIBRONECTIN_1; 1.
 CC PROSITE: PS00023; FIBRONECTIN_2; 1.
 CC PROSITE: PS00021; KRINGLE_1; 1.
 CC PROSITE: PS00070; KRINGLE_2; 1.
 CC PROSITE: PS50240; TRYPSIN_DOM; 1.
 CC PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
 KW Hydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen;
 KW Polymorphism; Disease mutation.
 FT SIGNAL 1 19
 FT CHAIN 20 372 ALPHA-FACTOR XIIA HEAVY CHAIN.
 FT CHAIN 373 615 ALPHA-FACTOR XIIA LIGHT CHAIN.
 FT CHAIN 354 362 BETA-FACTOR XIIA PART 1.
 FT CHAIN 373 615 BETA-FACTOR XIIA PART 2.
 FT DOMAIN 47 88 FIBRONECTIN TYPE-II.
 FT DOMAIN 94 131 EGF-LIKE 1.
 FT DOMAIN 133 173 FIBRONECTIN TYPE-I.
 FT DOMAIN 174 210 EGF-LIKE 2.

FT DOMAIN 217 295 KRINGLE.
 FT DOMAIN 296 349 PRO-RICH.
 FT DOMAIN 373 615 SERINE PROTEASE.
 FT CARBOHYD 109 109 O-LINKED (FUC).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC...).
 FT CARBOHYD 299 299 O-LINKED (POTENTIAL).
 FT CARBOHYD 305 305 O-LINKED (POTENTIAL).
 FT CARBOHYD 308 308 O-LINKED (POTENTIAL).
 FT CARBOHYD 328 328 O-LINKED (POTENTIAL).
 FT CARBOHYD 329 329 O-LINKED (POTENTIAL).
 Query Match 5.2%; Score 13; DB 1; Length 615;
 Best Local Similarity 100.0%; Pred.No. 1.5e-05; Indels 0; Caps 0;
 Matches 13; Conservative 0; Mismatches 0;
 QY 194 DACQDSGGPLVC 206
 |||||
 Db 557 DACQDSGGPLVC 569
 |||||
 Search completed: June 16, 2004, 15:14:01
 Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 15:10:47 ; Search time 46 Seconds
(without alignments)
1701.055 Million cell updates/sec

Title: US-10-006-116a-194

Perfect score: 248

Sequence: 1 MGLSIFLLICVLGLSQAATP.....GVVYICKYVDWIRMRNN 248

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	26.2	111	4 Q9UKR2	Q9ukr2 homo sapien
2	31	12.5	234	11 Q9CV76	Q9cv76 mus musculus
3	14	5.6	681	13 Q7ZT70	Q7zt70 lampetra ja
4	13	5.2	200	11 Q924U6	Q924u6 mus musculus
5	13	5.2	235	4 Q9N4E0	Q9n4e0 homo sapien
6	13	5.2	242	11 Q80VS4	Q80vs4 mus musculus
7	13	5.2	243	4 Q86VJ5	Q86vj5 homo sapien
8	13	5.2	246	11 Q883J01	Q883j01 mus musculus
9	13	5.2	247	13 Q9W7Q5	Q9w7q5 paralichthy
10	13	5.2	250	11 Q8CGR5	Q8cgr5 mus musculus
11	13	5.2	251	11 Q54854	Q54854 rattus norv
12	13	5.2	253	4 Q9WZB4	Q9wzb4 homo sapien
13	13	5.2	253	11 Q91Y82	Q91y82 mus musculus
14	13	5.2	267	6 Q9MZZ6	Q9mzz6 macaca fasc
15	13	5.2	277	5 Q96899	Q96899 scolopendra
16	13	5.2	300	4 Q96EF3	Q96ef3 homo sapien

17	13	5.2	320	13 Q7TOX2	Q7tox2 xenopus lae
18	13	5.2	371	11 Q8CJ16	Q8cj16 rattus norv
19	13	5.2	389	13 Q9PVX7	Q9pvx7 xenopus lae
20	13	5.2	395	4 Q9BZW1	Q9bzw1 homo sapien
21	13	5.2	445	11 Q8CJ17	Q8cj17 rattus norv
22	13	5.2	455	11 Q8CDR0	Q8cdr0 mus musculus
23	13	5.2	516	4 Q9BU99	Q9bu99 homo sapien
24	13	5.2	562	4 Q86VK8	Q86vk8 homo sapien
25	13	5.2	562	6 Q8SQ23	Q8sq23 sus scrofa
26	13	5.2	564	6 Q8MXB1	Q8mxb1 oryctolagus
27	13	5.2	597	11 Q35727	Q35727 mus musculus
28	13	5.2	609	11 Q80YC5	Q80yc5 mus musculus
29	13	5.2	615	4 Q81Z25	Q81zz5 homo sapien
30	13	5.2	616	6 Q97507	Q97507 sus scrofa
31	13	5.2	653	11 Q8VCS4	Q8vcs4 mus musculus
32	13	5.2	1524	13 Q91674	Q91674 xenopus lae
33	12	4.8	85	5 Q8MVL1	Q8mvl1 boltenia vi
34	12	4.8	155	5 Q9Y1K4	Q9y1k4 anopheles g
35	12	4.8	187	5 Q45045	Q45045 scirpophaga
36	12	4.8	253	5 Q8SX24	Q8sx24 drosophila
37	12	4.8	253	5 Q8MKZ1	Q8mkz1 drosophila
38	12	4.8	254	5 Q9XYV0	Q9xyv0 rhyzopertha
39	12	4.8	254	5 Q76520	Q76520 stomoxys ca
40	12	4.8	255	3 Q9Y7A9	Q9y7a9 metarhizium
41	12	4.8	256	5 Q25081	Q25081 hypoderma l
42	12	4.8	256	5 Q9XYV1	Q9xyv1 rhyzopertha
43	12	4.8	256	5 Q18599	Q18599 drosophila
44	12	4.8	258	5 Q9W5U8	Q9w5u8 drosophila
45	12	4.8	260	5 Q9V6P6	Q9v6p6 drosophila

ALIGNMENTS

RESULT 1

Q9UKR2 ID Q9UKR2 PRELIMINARY; PRT; 111 AA.
AC Q9UKR2, 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Kallikrein-like protein 5-related protein 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yousef G.M., Luo L., Diamandis E.P.;
RT "Identification of novel human kallikrein-like genes on chromosome 19q13.3-q13.4";
RL Anticancer Res. 79:2843-2852(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21121728; PubMed=10675891;
RA Diamandis E.P., Yousef G.M., Lou L.Y., Magklara A., Obiezu C.;
RT "The new kallikrein gene family: implications in carcinogenesis.";
RL Trends Endocrinol. Metab. 11:54-60(2000).
DR EMBL; AF135025; AAF06066.1; -;
DR HSSP; P00752; 1H1A.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004235; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001254; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 111 AA; 11984 MW; 3888A4295635D8D CRC64;

Query Match 26.2%; Score 65; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 2e-59;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLSIFLLLCVLGLSQAATPKIFNTECGRNSQPMQVGLFEGTSLRCSGVLIDHRWLTATA 60
 DB 1 MGLSIFLLLCVLGLSQAATPKIFNTECGRNSQPMQVGLFEGTSLRCSGVLIDHRWLTATA 60

QY 61 AHCSG 65
 DB 61 AHCSG 65

RESULT 2 Q9CV76

ID Q9CV76 PRELIMINARY; PRT; 234 AA.
 AC Q9CV76;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 2310008B01RIK protein (Fragment).
 GN 2310008B01RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staab P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; AK009217; BAB26143.1; -.
 DR HSP; P00763; IDPO.
 DR MEROPS; S01.020; -.
 DR MGP; MGI:1916761; 2310008B01RIK.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Protease; Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 234 AA; 25888 MW; 6D81E609BDD39110 CRC64;

Query Match 12.5%; Score 31; DB 11; Length 234;
 Best Local Similarity 100.0%; Pred. No. 1.1e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVCGSVLQGLVSWGSGVGPCGO 224
 DB 180 DACQDSGGPLVCGSVLQGLVSWGSGVGPCGO 210

RESULT 3 Q7ZT70

ID Q7ZT70 PRELIMINARY; PRT; 681 AA.
 AC Q7ZT70;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mannose-binding lectin associated serine protease-1.
 GN MASP-1.
 OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lethenteron.
 OX NCBI_TaxID=94989;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22593355; PubMed=12707349;
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsusita A., Takahashi M.,
 RA Matsushita M., Fujita T.;
 RT "Origin of Mannose-Binding Lectin-Associated Serine Protease (MASP)-1
 and MASP-3 Involved in the Lectin Complement Pathway Traced Back to
 the Invertebrate, Amphioxus."
 RL J. Immunol. 170:4701-4707(2003).
 DR EMBL; AB089265; BAC75884.1; -.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:oxidoreductase activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005529; P:sugar binding; IEA.
 DR GO; GO:0007157; P:trypsin activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR002086; Aldehyde dehydr.
 DR InterPro; IPR000152; Aax_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00084; sushi; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Lectin; Protease.
 SQ SEQUENCE 681 AA; 75277 MW; 27386FA117C1D437 CRC64;

Query Match 5.6%; Score 14; DB 13; Length 681;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 192 QDACCQDSGGPLV 205
 DB 622 QDACCQDSGGPLV 635


```
RESULT 4
Q924U6 PRELIMINARY; PRT; 200 AA.
ID Q924U6
AC Q924U6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine protease-like 1.
GN 1700036D21RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsui H., Takahashi T.;
RT "Mus musculus mRNA for serine protease-like gene spliced variant-1."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB047758; BAB63919.1; -.
DR HSSP; P00761; IANI.
DR MEROPS; S01.106; -.
DR MGD; MGI:1920586; 1700036D21RIK.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004235; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease
SQ SEQUENCE 200 AA; 22135 MW; 972959E4686BF603 CRC64;

Query Match 5.2%; Score 13; DB 11; Length 200;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVC 206
Db 128 DACQDSGGPLVC 140

RESULT 5
Q8N4E0 PRELIMINARY; PRT; 235 AA.
ID Q8N4E0
AC Q8N4E0
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RT Tissue=skin;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC034529; AAH34529.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004235; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.

Query Match 5.2%; Score 13; DB 11; Length 200;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVC 206
Db 128 DACQDSGGPLVC 140

RESULT 6
Q80VS4 PRELIMINARY; PRT; 242 AA.
ID Q80VS4
AC Q80VS4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to kallikrein 14 (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strauberg R.;
RT Tissue=Breast tumor;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044756; AAH44756.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004235; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
FT NON_TER 1
SQ SEQUENCE 242 AA; 26059 MW; A3F8A624DE481D36 CRC64;

Query Match 5.2%; Score 13; DB 11; Length 242;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CQDGGGGLVCGG 208
Db 191 CQDGGGGLVCGG 203

RESULT 7
Q86VJ5 PRELIMINARY; PRT; 243 AA.
ID Q86VJ5
AC Q86VJ5
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to D component of complement (Adipsin) (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

Query Match 5.2%; Score 13; DB 11; Length 242;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CQDGGGGLVCGG 208
Db 191 CQDGGGGLVCGG 203
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DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 247 AA; 26948 MW; DC4B647179DD972 CRC64;

Query Match          5.2%; Score 13; DB 13; Length 247;
Best Local Similarity 100.0%; Pred. No. 7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVCG 206
Db 194 DACQDSGGPLVCG 206
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RESULT 10
ID Q8CGR5 PRELIMINARY; PRT; 250 AA.
AC Q8CGR5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Glandular kallikrein KLK14.
GN KLK14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2325484; PubMed=12437987;
RA Olsson A.Y., Lundwall A.;
RT "Organization and evolution of the glandular kallikrein locus in Mus
RL Biochem. Biophys. Res. Commun. 299:305-311(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M., Mural R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EXBL; AY152433; AAN78421.1; -.
DR MGD; MGI:2447564; Kik14.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 250 AA; 27016 MW; F62FEBF2290FEBE8 CRC64;

Query Match          5.2%; Score 13; DB 11; Length 250;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CQDSDGGPLVCG 208
Db 199 CQDSDGGPLVCG 211
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RESULT 11
OS4854 PRELIMINARY; PRT; 251 AA.
ID OS4854
AC OS4854
DT 01-JUN-1998 (TrEMBLrel. 06, Created)

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DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DB Myelencephalon specific protease.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97477435; PubMed=9334391;
RA Scarlebrick I.A., Townner M.D., Isaacson P.J.;
RT "Nervous system-specific expression of a novel serine protease:
RT regulation in the adult rat spinal cord by excitotoxic injury.";
RL J. Neurosci. 17:8156-8168(1997).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF016269; AAC02300.1; -.
DR HSP; P00763; IDPO.
DR MEROPS; S01.236; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 251 AA; 28014 MW; E21967EF06CEBBF9 CRC64;

Query Match          5.2%; Score 13; DB 11; Length 251;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CQDSDGGPLVCG 208
Db 200 CQDSDGGPLVCG 212
|||||

RESULT 12
Q8WZB4 PRELIMINARY; PRT; 253 AA.
ID Q8WZB4
AC Q8WZB4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adipsin/complement factor D precursor (EC 3.4.21.46).
GN DF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ralle M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AJ313463; CAC48304.1; -.
DR HSP; P00761; IAN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0003817; F:complement factor D activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.

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DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HYDROLASE; Protease; Serine protease; Signal.
FT SIGNAL 1 8 POTENTIAL.
FT CHAIN 9 253 ADIPSIN/COMPLEMENT FACTOR D PRECURSOR.
SQ SEQUENCE 253 AA; 27033 MW; 78B06C209DEEA362 CRC64;

Query Match 5.2%; Score 13; DB 4; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 198 GDSGGPLVCGGVL 210
Db 206 GDSGGPLVCGGVL 218

RESULT 13
Q91Y82 PRELIMINARY; PRT; 253 AA.
AC Q91Y82;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neurosin (Protease, serine, 18).
GN PRS18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mitsu S., Yamaguchi N.;
RT "cDNA cloning and characterization of mouse brain specific serine
RT protease, Neurosin."
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB008928; BAB55605.1; -.
DR EMBL; BC031119; AAB31119.1; -.
DR HSSP; P00761; IAN1.
DR MEROPS; S01.236; -.
DR MGD; MGI:1343166; Prrs18.
DR GO; GO:0004263; P:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR HYDROLASE; Protease; Serine protease.
KW Hydrolyase;
SQ SEQUENCE 253 AA; 28329 MW; C5EF98C7EEF2FBC1 CRC64;

Query Match 5.2%; Score 13; DB 11; Length 253;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 196 CQSDSGPLVCGG 208
Db 200 CQSDSGPLVCGG 212

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RESULT 14
Q9MZ26 PRELIMINARY; PRT; 267 AA.
AC Q9MZ26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB046651; BAB03569.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.299; -.
DR GO; GO:0004263; P:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase;
SQ SEQUENCE 267 AA; 29516 MW; 69ACD18A0137APC7 CRC64;

Query Match 5.2%; Score 13; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 DACQDSGGPLVC 206
Db 159 DACQDSGGPLVC 171

RESULT 15
Q96899 PRELIMINARY; PRT; 277 AA.
AC Q96899;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen activator sPa.
OS Scolopendra subspinipes.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda; Scolopendra.
OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Scolopendra.
OX NCBI_TaxID=55038;
RN [1]
RP SEQUENCE FROM N.A.
RA Sohn Y.-D., You W.K., Kim K.Y., Chung K.H., Park D.-H.;
RT "Cloning of a cDNA for a novel plasminogen activator from a Korean
RT centipede Scolopendra."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; U79521; AAD00320.1; -.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.122; -.
DR GO; GO:0004263; P:chymotrypsin activity; IEA.
DR GO; GO:0008233; P:peptidase activity; IEA.

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DR GO: 0004295; F: trypsin activity; IEA.
DR GO: 0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro: IPR009003; Cys Ser trypsin.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; Tryp_SPC; 1.
DR PROSITE: PS0240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
SQ SEQUENCE 277 AA; 30172 MW; EC62F80C8CBB246C CRC64;

Query Match 5.2%; Score 13; DB 5; Length 277;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 DACQDSGGPLVC 206
|||
DB 212 DACQDSGGPLVC 224

Search completed: June 16, 2004, 15:15:00
Job time : 48 secs